

OM protein - protein search, using sw model	GenCore version 5.1.4_P5_4578			
Copyright (c) 1993 - 2003 Compugen Ltd.				
Run on: April 16, 2003, 08:59:57 ; Search time 26 Seconds				
Maximum DB seq length: 0 (without alignments)				
Post-processing: Minimum Match 0%	52.0.049 Million cell updates/sec			
Post-processing: Maximum Match 100%				
Database : BLOSUM62	KAVMVVEEPRKRGESFFGG 326			
Scoring table: Gapop 10.0 , Gapext 0.5				
Searched: 112892 seqs, 41476328 residues				
Total number of hits satisfying chosen parameters: 112892				
Minimum DB seq length: 0				
Maximum DB seq length: 200000000				
Post-processing: Minimum Match 0%				
Post-processing: Maximum Match 100%				
Database : SwissProt_40:*	Listing first 45 summaries			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query Match length	DB ID	Description
1	799.5	48.3	286	MIND_MESVI
2	792	47.9	282	MIND_CHLUV
3	694.5	42.0	269	MIND_GUTH
4	643	38.9	265	MIND_SYN3
5	523	31.6	268	MIND_BACSU
6	505.5	30.6	268	MIND_HELPY
7	500	30.3	268	MIND_HELPI
8	479	29.0	269	MIND_ECOLI
9	475.5	28.7	271	MIND_THEME
10	460	27.8	269	MIND_BUCAI
11	300	18.1	264	Y547_METJA
12	242	14.6	263	Y169_METJA
13	214	12.9	298	YLXH_BACSU
14	213	12.9	353	MRP_SINY3
15	211	12.8	364	MRP_AQUAE
16	209	12.6	368	MRP_HELPJ
17	205	12.5	368	MRP_HELPY
18	197.5	11.9	350	MRP_DEBRA
19	196.5	11.9	295	YH95_PYRAB
20	193.5	11.7	295	Y949_PYRHO
21	191	11.5	290	Y283_METJA
22	190	11.5	381	MRP_MCYTC
23	183.5	11.1	253	Y685_METJA
24	183	11.1	253	SOJ_BACSU
25	181	10.9	287	YQAB_PSEFR
26	177.5	10.7	383	MRP_MYCLE
27	173.5	10.5	271	NUEZ_HUMAN
28	173.5	10.5	369	MRP_ECOLI
29	165	10.0	257	Y823_METJA
30	164.5	9.9	267	PARA_CAUCA
31	164.5	9.9	275	NUB2_MOUSE
32	161	9.7	263	Y924_METJA
33	160.5	9.7	287	RCHL_HELMO

QY	225 CIPDPRMIVRUPTRMIGERMSVLDVCGSISGVIPEDSEVIRSTNRGFLVINK 284
Db	179 GIVEVKLVLVNPVPPDMIQKNDLISVVDQENLGIPLGAFLPEDTNVIVSTNRGQPLVINK 238
QY	285 PPTLAGLAEQAMRIVEQDSMKAIVVVEEPEKRG 319
Db	239 KLTLSGISEFNAARPLV--GRKEYLUNLETGNG 270
RESULT 2	
MIND	CHLWU
ID	_MIND_CHLWU
STANDARD;	
PRT;	282 AA.
AC	P56346;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Putative septum site-determining protein mind.
GN	MIND.
OS	Chloroplast.
OG	Eukaryota; Viridiplantae; Chlorophyta, Trebouxiophyceae, Chlorellales, Chlorellaceae; Chlorella; Chlorella, NCBI_TaxID=3077;
OX	
RN	
RP	SEQUENCE FROM N.A.
SP	SPTRN1.TAM C-77 / Tamya;
PC	MEDLINE=97303241; PubMed=9159184;
RX	Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S., RA
RA	Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T., Inamura A., Yoshinaga K., Sugura M., RA
RT	"Complete nucleotide sequence of the chloroplast genome from the green alga Chlorella vulgaris: the existence of genes possibly involved in chloroplast division.";
RT	Proc. Natl. Acad. Sci. U. S. A. '94. 91:5972 (1994);
CC	-- FUNCTION: ATPase required for the correct placement of the DIVISION SITE (BY SIMILARITY)
CC	-- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
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CC	--
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CC	--
CC	DR EMBL; AR001684; BAA57951.1; --
CC	DR Interpro; IPR000707; Atpase_Para.
CC	DR Pfam; PF00991; Para; 1.
CC	KW Cell division; Separation; ATP-binding; Chloroplast.
CC	FT NP_BIND 10 17 ATP (POTENTIAL).
CC	SEQUENCE 269 AA; 23455 MW; BC3C3B954E689EAC CRC64;
CC	--
CC	DR EMBL; AR001684; BAA57951.1; --
CC	DR Interpro; IPR000707; Atpase_Para.
CC	DR Pfam; PF00991; Para; 1.
CC	KW Cell division; Separation; ATP-binding; Chloroplast.
CC	FT NP_BIND 10 17 ATP (POTENTIAL).
CC	SEQUENCE 269 AA; 23455 MW; BC3C3B954E689EAC CRC64;
RESULT 3	
MIND	GUITH
ID	_MIND_GUITH
STANDARD;	
PRT;	269 AA.
AC	078436;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Putative septum site-determining protein mind.
GN	MIND.
OS	Guillardia theta (Cryptomonas phi)
OG	Chloroplast.
OC	Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX	NCBI_TaxID=55529;
RN	[1]
RP	SEQUENCE FROM N.A. PubMed=9929332;
RX	MECLINE=9912221;
RA	Douglas S.E., Penny S.L.;
RT	"The plastid genome of the cryptophyte alga, Guillardia theta: complete sequence and conserved synteny groups confirm its common ancestry with red algae."
RL	J. Mol. Evol. 48:236-244 (1999).
RX	-- FUNCTION: ATPase required for the correct placement of the DIVISION SITE (BY SIMILARITY).
CC	--
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CC	--
CC	DR EMBL; AR041468; AAC3521.1; --
CC	DR Interpro; IPR000707; Atpase_Para.
CC	DR Pfam; PF00991; Para; 1.
CC	KW Cell division; Separation; ATP-binding; Chloroplast.
CC	FT NP_BIND 10 17 ATP (POTENTIAL).
CC	SEQUENCE 269 AA; 23455 MW; BC3C3B954E689EAC CRC64;
RESULT 4	
QY	299 RIV-EQSMMAVVAEEPEKRGFF--SFFGG 326
Db	252 RLIGKQG...YFIDLSPQKMFQVQEFLG 280
QY	59 RIVVITSGKGGVKTITANVGLSARYGFSVAIDGLRNLDLGLGLENRNYTVE 118
Db	3 RIVVITSGKGGVKTITANVGLSARYGFSVAIDGLRNLDLGLGLENRNYTVE 62
QY	119 RIVVITSGKGGVKTITANVGLSARYGFSVAIDGLRNLDLGLGLENRNYTVE 178
Db	63 VLSGCERLQALIKDKPQPNLVMIAAQNPNK--DSVTEQMKFVNLL--VNNTYDYL 116
QY	179 IIDCPAGIDAGFTITAPANEAVLVTIDPITALRDAAPVTSLECTGIPDMIVNRP 238
Db	117 IIDCPAGIDAGFTITAPANEAVLVTIDPITALRDAAPVTSLECTGIPDMIVNRP 176
QY	239 DMIGKEDMMSVLDVQEMIGLISLGIVIPEDSEVIRSTNRGFLVINK 298
Db	177 QMVKANDMSVLDVRETAIAFLIGNVIEDECIVSINGRERIVLVEGLSLGAFHETAC 236
QY	299 RIVVQDSMVAWVTEERPPRG 319
Db	237 RL--DGQETEFLDLQSYSRG 254
MIND SYN3	
QY	192 DMIGKEDMMSVLDVQEMIGLISLGIVIPEDSEVIRSTNRGFLVINK 251

ID MIND SYN3 STANDARD; PRT; 266 AA.
 AC Q55900; 055900; 15-JUL-1998 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Septum site-determining protein mind (Cell division inhibitor mind).
 GN MIND OR SL0289.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxId=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127539; PubMed=8590279;
 RA Kaneko T.; Tanaka A.; Sato S.; Kotani H.; Sazuka T.; Miyajima N.;
 RT Sugiura M.; Tabata S.;
 "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 region from map positions 64% to 92% of the genome.",
 DNA Res. 2:153-166(1995).
 CC -!- FUNCTION: ATPase required for the correct placement of the
 DIVISION SITE. CELL DIVISION INHIBITORS MINC AND MIND ACT IN
 CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
 POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
 CELL TO DESTABILIZE FTSZ FILAMENTS THAT HAVE FORMED BEFORE THEY
 MATURE INTO POLAR Z RINGS (BY SIMILARITY).
 CC -!- SUBUNIT: INTERACTS WITH MINC AND FTSZ (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
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 DR EMBL; D64005; BAA10662.1; -.
 DR InterPro; IPR000707; ATPase_Para.
 DR InterPro; IPR000392; NitrogenaseII.
 DR Pfam; PF00142; ferA_NiFH; 1.
 DR Pfam; PF00991; Para; 1.
 DR Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 PT NP BIND SEQUENCE 266 AA; 29407 MW; 4BC37880F088C9BF CRC64;
 SQ

Query Match 38.9%; Score 643; DB 1; Length 266;
 Best Local Similarity 52.8%; Pred. No. 2.4e-44;
 Matches 130; Conservative 51; Mismatches 59; Indels 6; Gaps 2;
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 DR EMBL; D64005; BAA10662.1; -.
 DR InterPro; IPR000707; ATPase_Para.
 DR InterPro; IPR000392; NitrogenaseII.
 DR Pfam; PF00142; ferA_NiFH; 1.
 DR Pfam; PF00991; Para; 1.
 DR Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 PT NP BIND SEQUENCE 266 AA; 29407 MW; 4BC37880F088C9BF CRC64;
 SQ

Query Match 38.9%; Score 643; DB 1; Length 266;
 Best Local Similarity 52.8%; Pred. No. 2.4e-44;
 Matches 130; Conservative 51; Mismatches 59; Indels 6; Gaps 2;
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 DR EMBL; D64005; BAA10662.1; -.
 DR InterPro; IPR000707; ATPase_Para.
 DR InterPro; IPR000392; NitrogenaseII.
 DR Pfam; PF00142; ferA_NiFH; 1.
 DR Pfam; PF00991; Para; 1.
 DR Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 PT NP BIND SEQUENCE 266 AA; 29407 MW; 4BC37880F088C9BF CRC64;
 SQ

Query Match 31.6%; Score 523; DB 1; Length 268;
 Best Local Similarity 41.1%; Pred. No. 9.4e-35; Mismatches 77; Indels 14; Gaps 7;
 Matches 111; Conservative 68; Mismatches 77; Indels 14; Gaps 7;
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 DR EMBL; D64005; BAA10662.1; -.
 DR InterPro; IPR000707; ATPase_Para.
 DR InterPro; IPR000392; NitrogenaseII.
 DR Pfam; PF00142; ferA_NiFH; 1.
 DR Pfam; PF00991; Para; 1.
 DR Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 PT NP BIND SEQUENCE 268 AA; 29407 MW; 6665B9F693F58A9B CRC64;
 SQ

Query Match 31.6%; Score 523; DB 1; Length 268;
 Best Local Similarity 41.1%; Pred. No. 9.4e-35; Mismatches 77; Indels 14; Gaps 7;
 Matches 111; Conservative 68; Mismatches 77; Indels 14; Gaps 7;
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 DR EMBL; D64005; BAA10662.1; -.
 DR InterPro; IPR000707; ATPase_Para.
 DR InterPro; IPR000392; NitrogenaseII.
 DR Pfam; PF00142; ferA_NiFH; 1.
 DR Pfam; PF00991; Para; 1.
 DR Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 PT NP BIND SEQUENCE 268 AA; 29407 MW; 6665B9F693F58A9B CRC64;
 SQ

Query Match 61.0%; Score 120; DB 1; Length 268;
 Best Local Similarity 41.1%; Pred. No. 9.4e-35; Mismatches 77; Indels 14; Gaps 7;
 Matches 111; Conservative 68; Mismatches 77; Indels 14; Gaps 7;
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 CC
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 DR EMBL; D64005; BAA10662.1; -.
 DR InterPro; IPR000707; ATPase_Para.
 DR InterPro; IPR000392; NitrogenaseII.
 DR Pfam; PF00142; ferA_NiFH; 1.
 DR Pfam; PF00991; Para; 1.
 DR Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 PT NP BIND SEQUENCE 268 AA; 29407 MW; 6665B9F693F58A9B CRC64;
 SQ

ID MIND_BACSU STANDARD; PRT; 268 AA.
 AC Q01464; 001464; 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Septum site-determining protein mind (Cell division inhibitor mind).
 GN MIND OR DIVIVB.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxId=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RX MEDLINE=93015732; PubMed=1400225;
 RA Varley A.W.; Stewart G.C.;
 RT "The divIVB region of the *Bacillus subtilis* chromosome encodes
 homologs of *Escherichia coli* septum placement (minCD) and cell shape
 (minBCD) determinants";
 J. Bacteriol. 174:6729-6742(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RA Lee S.; Price C.W.;
 RT "The minCD locus of *Bacillus subtilis* lacks the minE determinant that
 provides topological specificity to cell division.>";
 Mol. Microbiol. 7:601-610(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93015731; PubMed=8459776;
 RA Levin P.A.; Margolis P.S.; Setlow P.; Losick R.; Sun D.;
 RT "Identification of *Bacillus subtilis* genes for septum placement and
 shape determination.>";
 J. Bacteriol. 174:6717-6728(1992).
 CC -!- FUNCTION: ATPase required for the correct placement of the
 DIVISION SITE. CELL DIVISION INHIBITORS MINC AND MIND ACT IN
 CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
 POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
 CELL TO DESTABILIZE FTSZ FILAMENTS THAT HAVE FORMED BEFORE THEY
 MATURE INTO POLAR Z RINGS (BY SIMILARITY).
 CC -!- SUBUNIT: INTERACTS WITH MINC AND FTSZ (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.
 CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
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 CC
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 DR EMBL; M95502; AAA22609.1; -.
 DR EMBL; M9543; AAA22401.1; -.
 DR EMBL; Z29918; CAB14759.1; -.
 DR PIR; S31205; S31205.
 DR PIR; G45229; G45239.
 DR PIR; F45240; F45240.
 DR Sublist; BGI0330; mind.
 DR InterPro; IPR000707; ATPase_Para.
 DR Pfam; PF00991; Para; 1.
 DR Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 PT NP BIND SEQUENCE 268 AA; 29407 MW; 6665B9F693F58A9B CRC64;
 SQ

Query Match 61.0%; Score 120; DB 1; Length 268;
 Best Local Similarity 41.1%; Pred. No. 9.4e-35; Mismatches 77; Indels 14; Gaps 7;
 Matches 111; Conservative 68; Mismatches 77; Indels 14; Gaps 7;
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 CC
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 DR EMBL; M95502; AAA22609.1; -.
 DR EMBL; M9543; AAA22401.1; -.
 DR EMBL; Z29918; CAB14759.1; -.
 DR PIR; S31205; S31205.
 DR PIR; G45229; G45239.
 DR PIR; F45240; F45240.
 DR Sublist; BGI0330; mind.
 DR InterPro; IPR000707; ATPase_Para.
 DR Pfam; PF00991; Para; 1.
 DR Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 PT NP BIND SEQUENCE 268 AA; 29407 MW; 6665B9F693F58A9B CRC64;
 SQ

Query Match 61.0%; Score 120; DB 1; Length 268;
 Best Local Similarity 41.1%; Pred. No. 9.4e-35; Mismatches 77; Indels 14; Gaps 7;
 Matches 111; Conservative 68; Mismatches 77; Indels 14; Gaps 7;
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 or send an email to license@isb-sib.ch).
 CC
 CC
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 DR EMBL; M95502; AAA22609.1; -.
 DR EMBL; M9543; AAA22401.1; -.
 DR EMBL; Z29918; CAB14759.1; -.
 DR PIR; S31205; S31205.
 DR PIR; G45229; G45239.
 DR PIR; F45240; F45240.
 DR Sublist; BGI0330; mind.
 DR InterPro; IPR000707; ATPase_Para.
 DR Pfam; PF00991; Para; 1.
 DR Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 PT NP BIND SEQUENCE 268 AA; 29407 MW; 6665B9F693F58A9B CRC64;
 SQ

DR Pfam; PF00991; ParA; 1.
 KW Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 FT NP BIND 10 17 AIP (POTENTIAL).
 SO SEQUENCE 268 AA; 29265 MW; 1F479C18TA201A63 CRC64;
 Query Match 30.3%; Score 500 5; DR 1; Length 269;
 Best Local Similarity 39.8%; Pred. No. 5.9.e-33;
 Matches 109; Conservative 65; Mismatches 81; Indels 19; Gaps 5;
 QY 60 IIVITSGKGVGKVTTTANGLSILARYGFSVVA1DADIGLNRNNDLLGLENRNYTCVEV 119
 DB 4 WTTTSGKGVGKVTTTANGLAIGLRSQEVKVAVDFDGLRNLDMLGLENRIVDWDV 63
 QY 120 INGCRDQDQLVDRKWSNPELIGISKPSKLPWFGGKALFWMDALKTRPESGSPDTI 179
 DB 64 MERNQNLNSQALITDTRKTNLFLASOSKDNILKEVIA-LINALR---ADFDYL 117
 QY 180 IDCAGDAGFITAATPANEAVLWTPDTALPDRVGLGEGDGI-----DTMI 232
 DB 118 IDSPAGTESGEFHATLHDALMVVTPEVSSLRSDRVGIDAKSNPAKSSEVHEHLI 177
 QY 233 VNRVFTDMIKGEDMMSVLDVQEMGIGLUSLGVVPDSEVIRSTORGFLVLNKOPTLAGIA 292
 DB 178 INRKEVLMANGEMISIREVKICLPLGIGTPEHHTISATWKGEPVI-PRCESSKA 235
 QY 293 FEQAAWRLVQDSMMAVMMVEEPKRGFRSPFGG 326
 DB 236 YQRITTPRILGEE---VEVEFKAKRGFFSALKG 265
 RESULT 8
 MIND_ECOLI STANDARD PRT; 269 AA.
 ID MIND_ECOLI STANDARD PRT; 269 AA.
 AC P18157;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Septum site-determining protein mind (cell division inhibitor mind).
 DE MIND OR BL175 OR Z1937 OR ECS1169.
 OS Escherichia coli, and
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia;
 OX NCBI_TaxID=562, 83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89136010; PubMed=2645057;
 RA de Boer P.A.J.; Crossley R.E.; Rothfield L.I.;
 RT "A division inhibitor and a topological specificity factor coded for
 by the minicell locus determine proper placement of the division
 septum in *E. coli*";
 RL Cell 56:641-649(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG165;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R.; Plunkett G. III; Bloch C.A.; Perna N.T.; Burland V.;
 RA Riley M.; Collado-Vides J.; Glasner J.D.; Rode C.K.; Mayhew G.F.;
 RA Gregor J.; Davis N.W.; Kirkpatrick H.A.; Goeden M.A.; Rose D.J.;
 RA Mau B.; Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.;"
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061302; PubMed=8905232;
 RA Oshima T.; Aiba H.; Baba T.; Fujita K.; Hayashi K.; Honjo A.;
 RA Ikemoto K.; Inada T.; Itoh T.; Kojihara M.; Yamai K.; Kasihara K.;
 RA Kimura S.; Kiragawa M.; Makino K.; Masuda S.; Miki T.; Mitochi K.;
 RA Mori H.; Motomura K.; Nakamura Y.; Nishimoto H.; Nishio Y.; Saito N.;
 RA Sampei G.; Seki Y.; Tagami H.; Takemoto K.; Wada C.; Yamamoto Y.;
 RA Yano M.; Horiochi T.;
 RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome"
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RT DNA Res. 3:137-155(1996).
 RN [4]
 RQ SEQUENCE FROM N.A.
 RC STRAIN=Q157:H7 / ED1933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T.; Plunkett G. III; Burland V.; Mau B.; Glasner J.D.;
 RA Rose D.J.; Mayhew G.F.; Evans P.S.; Gregor J.; Kirkpatrick H.A.;
 RA Postle G.; Hackett J.; Klink S.; Boutin A.; Shao Y.; Miller L.;
 RA Grotbeck E.J.; Davis N.W.; Lin A.; Dimalanta E.T.; Potamitis K.;
 RA Apodaca J.; Anantharaman T.S.; Lin J.; Yen G.; Schwartz D.C.;
 RA Welch R.A.; Blattner F.R.;
 RQ "Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.";
 RL Nature 409:529-533(2001).
 RN [5]
 RQ SEQUENCE FROM N.A.
 RC STRAIN=Q157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T.; Makino K.; Ohnishi M.; Kurukawa K.; Ishii K.; Yokoyama K.;
 RA Han C.-G.; Ohtsubo E.; Nakayama K.; Murata T.; Tanaka M.; Tobe T.;
 RA Iida T.; Takami H.; Honda T.; Sasakawa C.; Ogasawara N.; Yasunaga T.;
 RA Kuhara S.; Shiba T.; Hattori M.; Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 RN [6]
 RQ SEQUENCE OF 1-12;
 RC STRAIN=K12 / EMG22;
 RX MEDLINE=91443975; PubMed=9298646;
 RA Link A.J.; Robison K.; Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of *Escherichia coli* K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 RN [7]
 RP FUNCTION_ AND MUTAGENESIS.
 RX MEDLINE=92097557; PubMed=1836760;
 RA de Boer P.A.J.; Crossley R., Hand A.P.; Rothfield L.I.;
 RT "The Mind protein is a membrane ATPase required for the correct
 placement of the *Escherichia coli* division site.";
 RL EMBO J. 10:4371-4380(1991).
 RN [8]
 RP CHARACTERIZATION.
 RX MEDLINE=93238467; PubMed=10220403;
 RA Raskin D.M.; de Boer P.A.;
 RT "Rapid pole-to-pole oscillation of a protein required for directing
 division to the middle of *Escherichia coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:4971-4976(1999);
 CC -- FUNCTION: ATPase REQUIRED FOR THE CORRECT PLACEMENT OF THE
 DIVISION SITE. CELL DIVISION INHIBITORS MIND AND MIND ACT IN
 CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
 POLAR Z RING SEPTUMS RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
 CELL TO DESTABILIZE FISSE FILAMENTS THAT HAVE FORMED BEFORE THEY
 CC MATURE INTO POLAR Z RINGS.
 CC -- SUBUNIT: INTERACTS WITH MINC AND FISZ.
 CC -- SUBCELLULAR LOCATION: Inner membrane associated.
 CC -- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY
 CC
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 CC or send an email to license@sb-sib.ch).
 CC
 DR EMBL; J03153; AAB59062.1; -.
 DR EMBL; AE02216; AAC74259.1; -.
 DR EMBL; D0751; BAA6009.1; -.
 DR EMBL; D90152; BAA36022.1; -.
 DR EMBL; AE00334; AAG56026.1; -.
 DR EMBL; AP002555; BAB35092.1; -.
 DR PIR; B1877; C8CCID.
 DR SWISS-2DPAGE; P18197; COLI.

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 CC -----
 DR EMBL; AP001119; BAB13034.1; -.
 DR InterPro; IPR000707; ATPase_Para.
 DR Pfam; PF00991; Para; 1.
 DR Ptam; PF03374; ArsA_ATPase; 1.
 KW Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 FT INIT_MET 0 BY SIMILARITY.
 NP_BIND FT SEQUENCE 9 16 ATP (POTENTIAL)
 NP_BIND 269 AA; 29805 MW; 4FDD56454C827 CRC64;
 NP_BIND DR EMBL; UG7504; AAB9859.1; -.
 NP_BIND DR TIGR; MU0547; -.
 NP_BIND DR InterPro; IPR000707; ATPase_Para.
 NP_BIND DR Pfam; PF00991; Para; 1.
 NP_BIND KW Hypothetical protein; ATP-binding; Complete proteome.
 NP_BIND FT SEQUENCE 13 21 ATP (POTENTIAL)
 NP_BIND 264 AA; 27737 MW; B9AF5108CD0CEC3 CRC64;
 NP_BIND SQ -----
 Query Match 18.1%; Score 300; DB 1; Length 264;
 Best Local Similarity 30.5%; Pred. No. 6e-17;
 Matches 82; Conservative 57; Mismatches 104; Indels 26; Gaps 6;
 QY 59 PIVVITSGKGGVGGTTTANVGLSALARVGFSAIDGLRNLIDJGLENRVNTCVE 118
 2 RIVVITSGKGGVGGKTTSSAIGTGLAQKOKTKTVIDFDIGLRNLIDJGLENRVYDFIN 61
 Db 119 VINGCRLQALVVKRNSNFEELCISKPPSKLPMGG- KALEMLVDAKTRPESPD 176
 62 VIQGATLQAIKTKTNNFLPASOTRDKAQTTRGVERKLTET----- FNNFD 114
 QY 177 FLLIDCPAGIDAGFTAITPANEAVLVTPTDIALRDRVGLCEDGIRDIK----- 230
 115 FICCSPPAGIETGAILAIVFADAEITINPEVNSVSSRDRGIGIISKSNSKAENKTPIK 174
 Db 231 --MIVNVRVRTDMIKEDMMSVLDVQEMIGLISLIGVTPEDSEVIRSTNRGFLVUNPPTL 288
 . 175 EYLLLTTRYNPPVKGEMLSMVTDLQIPIGVIPEDQSVLRAASNQGESILCINH 233
 - QY 289 AGLAAFEQAAWRI:VQDSKMAVMEVEEPKRGFSEFG 325
 234 AGCAVSDTNRLIGEE- RHFRTFTEEKSFLLRIFG 268
 Db -----
 RESULT 11
 Y547 - METJA STANDARD; PRT; 264 AA.
 AC 057967;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 35, Last sequence update)
 DE Hypothetical ATP-binding protein MJ0547.
 GN MJ0547.
 OS Methanococcus jannaschii.
 OC Archaea; Buryarchaeota; Methanococci; Methanococcales;
 OC Methanococcaceae; Methanococcaceae;
 OC Methanococcaceae; Methanococcaceae;
 RN [1] NCBI_TaxID=2190;
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=9637799; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kikuchi E.F., Weinstock G.K., Merrick J.M., Glodek A.,
 RA Scott J.L., Geohagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Cottrell M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.",
 RL Science 273:1058-1073 (1996).
 CC -----
 --!- SIMILARITY: HIGH, TO M.JANNASCHII MJ0547, SOME, TO MJ0410 AND
 TO MJ024.

CC -----
 CC !- SIMILARITY: SOME, TO PROKARYOTIC MIND AND TO THE MRP FAMILY.
 CC -----
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 CC -----
 DR EMBL; UG7504; AAB9859.1; -.
 DR TIGR; MU0547; -.
 DR InterPro; IPR000707; ATPase_Para.
 DR Pfam; PF00991; Para; 1.
 DR Ptam; PF03374; ArsA_ATPase; 1.
 KW Cell division; Separation; ATP-binding; Membrane; Complete proteome.
 FT INIT_MET 0 BY SIMILARITY.
 NP_BIND FT SEQUENCE 9 16 ATP (POTENTIAL)
 NP_BIND 264 AA; 27737 MW; B9AF5108CD0CEC3 CRC64;
 NP_BIND SQ -----
 Query Match 18.1%; Score 300; DB 1; Length 264;
 Best Local Similarity 30.5%; Pred. No. 6e-17;
 Matches 82; Conservative 57; Mismatches 104; Indels 26; Gaps 6;
 QY 61 WVITSGKGGVGGKTTTANVGLSALARVGFSAIDGLRNLIDJGLENRVNTCVEI 120
 9 IATIASKGKGTKTTISANLAVLAKGFKKAVLDAKIAMNLELIMGLEGK----- PVT 62
 Db 121 NGCRLQALVVKRNSNFEELCISKPPSKLPMG--- PGGKALEWVDAKTRPESPD 175
 63 LNDVLAGSKADIKATIYEGPEGIVL----- IPAGVSLEKFRRAPEKEKLEVIAHD-LV 115
 QY 176 DFLIDCPAGIDAGFTAITPANEAVLVTPTDIALRDRVGLCEDGIRDIMKVN 235
 116 ELLIDCPAGIETGAILAIVFADAEITINPEVNSVSSRDRGIGIISKSNSKAENKTPIK 175
 Db 236 VRTDMIKEDMMSVLDVQEMIGLISLIGVTPEDSEVIRSTNRGFLVUNPPTL 295
 176 VSNESTE---LGKVAIETILEPVNIVGVPEDFHVRAAAGFGLPLVIVIFPDSPAQATME 231
 QY 296 AANRLVQDSKMAVMEVEEPKRGFSEFG 324
 Db 232 IAAKLIG---AKYEAQKLYKESFISKE 256

 RESULT 12
 Y169 - MEJJA STANDARD; PRT; 263 AA.
 ID Y169_MEJJA
 AC 057633;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical ATP-binding protein MJ0169.
 GN MJ0169.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanococcaceae; Methanococcaceae;
 OC Methanococcaceae; Methanococcaceae;
 RN [1] NCBI_TaxID=2190;
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=9637799; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kikuchi E.F., Weinstock G.K., Merrick J.M., Glodek A.,
 RA Scott J.L., Geohagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.",
 RL Science 273:1058-1073 (1996).
 CC -----
 --!- SIMILARITY: HIGH, TO M.JANNASCHII MJ0547, SOME, TO MJ0410 AND
 TO MJ024.

CC -- SIMILARITY: SOME, TO PROKARYOTIC MIND AND TO THE MRP FAMILY.

CC

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CC

DR EMBL: U67474; AAB98154.1; -

DR TIGR: MJ169; -

DR InterPro: IPR00707; ATPase_Para

DR Pfam: PF00991; ParaA; 1

KW Hypothetical protein; ATP-binding; Complete proteome.

FT NP_BIND 10

FT SEQUENCE 263 AA; 28950 MW; 293PBE88EE7ZACF4 CRC64;

OY Query Match 14.6%; Score 242; DB 1; length 263.

Best Local Similarity 29.3%; Pred No. 2 5e-12;

Matches 77; Conservative 59; Mismatches 99; Indels 28; Gaps 9;

OY 60 IWTISGKGWGVKTTITANVGLSLARYGIVSWAADDAGLRLRNIDLLGLENVNNTCEV 119

Db 5 LITASGGGGVGGKTTITASIAVAVLAKGKVLADIDGDSMANIGLFLNNEKKA-KPSLHEV 63

OY 120 INGDCBLDQALVR--KRSNFEFLCISKPRSLKPLPMFGGGKALEWLVDAALKTRPREGSPD 176

Db 64 LS---EEADAVRDAIYKHKTGKVNL---PTSLSGLEGYKKSDFDIDLPDVNEVADDF-D 113

OY 177 FIIIDCPAGIDFATITPANEAVLVTIDPITALRDAADPRTGVLFCGIRDIMKTMVNRV 236

Db 114 YVITDAPAGLNREMATHATLADKLLWVPEMPSIDIAVRLKESAMAGTPMGWLNRV 173

OY 237 PTMVKMGRPMMSVLSVQEMGLSLLGIVPIDESEVIRSTNRGFRIV..LNKEPTTLAGLAF 293

Db 174 GRDF-GE- MGRPEIEMIJKGVIVNVEVPEPK 316

OY 294 EOANWLVEDQSMKAVNVEEPK 316

Db 224 -QYMKLASSIATAGVPIYIEDIK 245

RESULT 1³

VLXH BACSU STANDARD; PRT; 298 AA.

ID YLXH BACSU STANDARD; PRT; 298 AA.

AC P40742;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein YLXH.

GN YLXH.

OS *Bacillus subtilis*.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

OX NCBI_TaxId:1423;

RN [1] SEQUENCE FROM N A.

RN MEDLINE=95078462; PUBMED=798014;

RA Kirsch M.L., Carpenter P.R., Ordal G.W.;

RT "A putative ATP-binding protein from the che/fla locus of *Bacillus subtilis*";

RL DNA Seq. 4:271-275 (1994)

RN [2] STRAIN=168;

RN MEDLINE=98044031; PUBMED=9194377;

RA Azevedo V., Bertero M.G., Bessieres P., Rojotin A., Borchert S.,

RA Borrisse J., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galeron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Guillepi G., Guy B.J., Haga K., Halech J., Harwood C.P., Renaut A.,

RA Hibert H., Hollsppel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kishihara Y., Klarr-Blanchard M., Klein R.,

RA Kobayashi Y., Kottner P., Konings-van G., Krogh S., Kumano M.,

RA Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Lee S.M., Levine A., Liu H., Masuda M., Muel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moeti D., Nakai S., Noback M.,

RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Presecan E., Puig C., Purnelle B., Rapoport G., Ray M., Reynolds S.,

RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Toonon A.,

RA Tosato V., Uchiyama S., Vandenoel M., Vanlier F., Vassarotti A.,

RA Viari A., Wambutt R., Wedder E., Weitzenegger T.,

RA Winters P., Wipar A., Yamamoto H., Yamane K., Yasumoto K., Yara K.,

RA Yoshida K., Yoshioka H.F., Zumstein E., Yoshikawa H., Danchin A.,

RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*," Nature 330:249-256 (1991)

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DR EMBL: X73682; CAB62034.1; -

DR InterPro: IPR00707; ATPase_Para

DR Pfam: PF00991; ParaA; 1

KW Hypothetical protein; ATP-binding; Complete proteome.

FT NP_BIND 39

FT SEQUENCE 298 AA; 33160 MW; AF6FF71:PF3C1C072 CRC64;

OY Query Match 12.9%; Score 214; DB 1; length 298,

Best Local Similarity 25.2%; Pred No. 5.1e-10;

Matches 76; Conservative 56; Mismatches 119; Indels 50; Gaps 10;

OY 32 VNNPSRSRSPRSVQFNPK--PELAGETPRWVITSGKGVGKTTTANVGLSLARYGFS 89

Db 3 MNRYDQATLRAKMEKOPVLPVYQSKAKTLAVISGKGVGKSNITLNMALQDKGK 62

OY 90 WVAADAGLRLRNIDLLGLENVNNTCEVINGDERRDQLAVLVRDKRWSWSEELLISKRS 149

Db 63 VLLDLDIGNGNDILIG--NSSSATIDVDRKQLS--

OY 150 KLPNGF---GGALE-----WLVDALKTRPREGSP-DFIIDCPAGIDFATIT 195

Db 103 VGPKGRLVYISGSGTGLDVMFQDQKWRKWTFFANELSHALSQDFYVLFDMGAGLSKBOLPFL 162

OY 196 PANEAVLVTIDPITALPDA-DFVTLGELERDGFIDKIMIVRVPFTMKGDDMS----- 248

Db 163 SAEDLILITTPERTAIMDAYSIAVHLVTEENLMSMVAVAPCR_PQEGI:DAFPN:SPTRI 221

OY 249 .-VLDVQEMGLSLLGIVPIDESEVIRSTNRGFLVNLKPTPLAGLAFQAWPRIVEQDM 306

Db 222 HPLIVC---WQAGSVSDTIVSVAVEQFFPISQAKASRVEFLADALFERET 277

OY 307 K 307

Db 278 R 278

RESULT 14

MRP_SYN3 STANDARD; PRT; 353 AA.
 ID MRP_SYN3 STANDARD; PRT; 353 AA.
 AC P53531;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE MRP OR SDR0067.
 GN MRP OR AQ-737.
 OS Synechocystis sp. (strain PCC 6803)
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxId=1148;
 RN [1]-
 RP SEQUENCE FROM N.A.
 PX MEDLINE-96127529; PubMed-8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.,
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 region from map positions 64% to 92% of the genome.",
 RL DNA Res. 2:153-166(1995).
 CC --! SIMILARITY: BELONGS TO THE MRP/NBP35 FAMILY OF ATP-BINDING
 PROTEINS.
 CC
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 CC
 DR EMBL; D64001; BAA02971; --.
 DR InterPro; IPR002744; DUF59.
 DR InterPro; IPR000808; MRP_Family.
 DR Pfam; PF01883; DUF59; 1.
 DR PROSITE; PS01215; MRP; 1.
 KW ATP-binding; Complete proteome.
 FT NP_BIND 105 112 ATP (POTENTIAL).
 SEQUENCE 353 AA; 37131 MW; 891DC0B247113841 CRC64;

Query Match 12.9%; Score 213; DB 1; Length 353;
 Best Local Similarity 26.1%; Pred. No. 7.7e-10;
 Matches 82; Conservative 55; Mismatches 115; Indels 62; Gaps 12;

Qy 23 KTLISSLSPRFVNNPNSRSPSPRSPVSLQFFNRKPLAGETPRPWVITSGKGVGKTTANGLS 82
 Db 76 RVTABTPQKSLPDRQS-----VQGVENIATASSGKGSGVGKSTVAAVNAVA 121
 Qy 83 LARQFSVVAIDADLGLRNLDDLGLENFVNVTVEVINGDGRLDALVRLRKRWSNFELL 142
 Db 122 LAQTCGAVGVLDAIDYQPNAPTMGLGSG---AAVQVQNS---PQCEVLEPVF NHGIK 172
 Qy 143 CISRSKSLPKMGF-----GGKALEWLWDLALKTRPE-GSPDRPPIIDCPAGI-DAGF 190
 Db 173 MVS-----MGEVLDPDPQVWGPMLNGIIPQFLQVNVWALDYLIVDRMPPGFDQAL 225
 Qy 191 -ITAIPANEAVLVTTPDITALRDADRVTLGELUCDGPGRDKITVN-----VPTDMIK 242
 Db 226 TLRQSPVPMAGAVITVTPVQLSLLDARPGI-KMFDQMGKGVNLGVENMSYFIPDLDPRQYD 285
 Qy 243 -----GDMMSVLDQCEMGLSLIGVIPEDSESVRSTNRGPPLVNLKPPILAGLAPEQA 296
 Db 286 LFGSGGGERKASKELNV-----PLLGCVPLEIGLRBGGDKGVPIVVSQPSASAKALTAI 339
 Qy 297 AMRUEQDSKAVM 310
 Db 340 AKQIAGKVSMALV 353

SEQUENCE FROM N.A.
 RP MEDLINE-96127529; PubMed-8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.,
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 region from map positions 64% to 92% of the genome.",
 RL DNA Res. 2:153-166(1995).
 CC --! SIMILARITY: BELONGS TO THE MRP/NBP35 FAMILY OF ATP BINDING
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 CC
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 CC
 DR EMBL; AB000705; AAC06915.1; --.
 DR InterPro; IPR002744; DUF59.
 DR Pfam; PF01883; DUF59; 1.
 DR PROSITE; PS01215; MRP; 1.
 KW ATP-binding; Complete proteome.
 FT NP_BIND 120 127 ATP (POTENTIAL).
 SEQUENCE 364 AA; 39492 MW; 320AE95C91A272A CRC64;

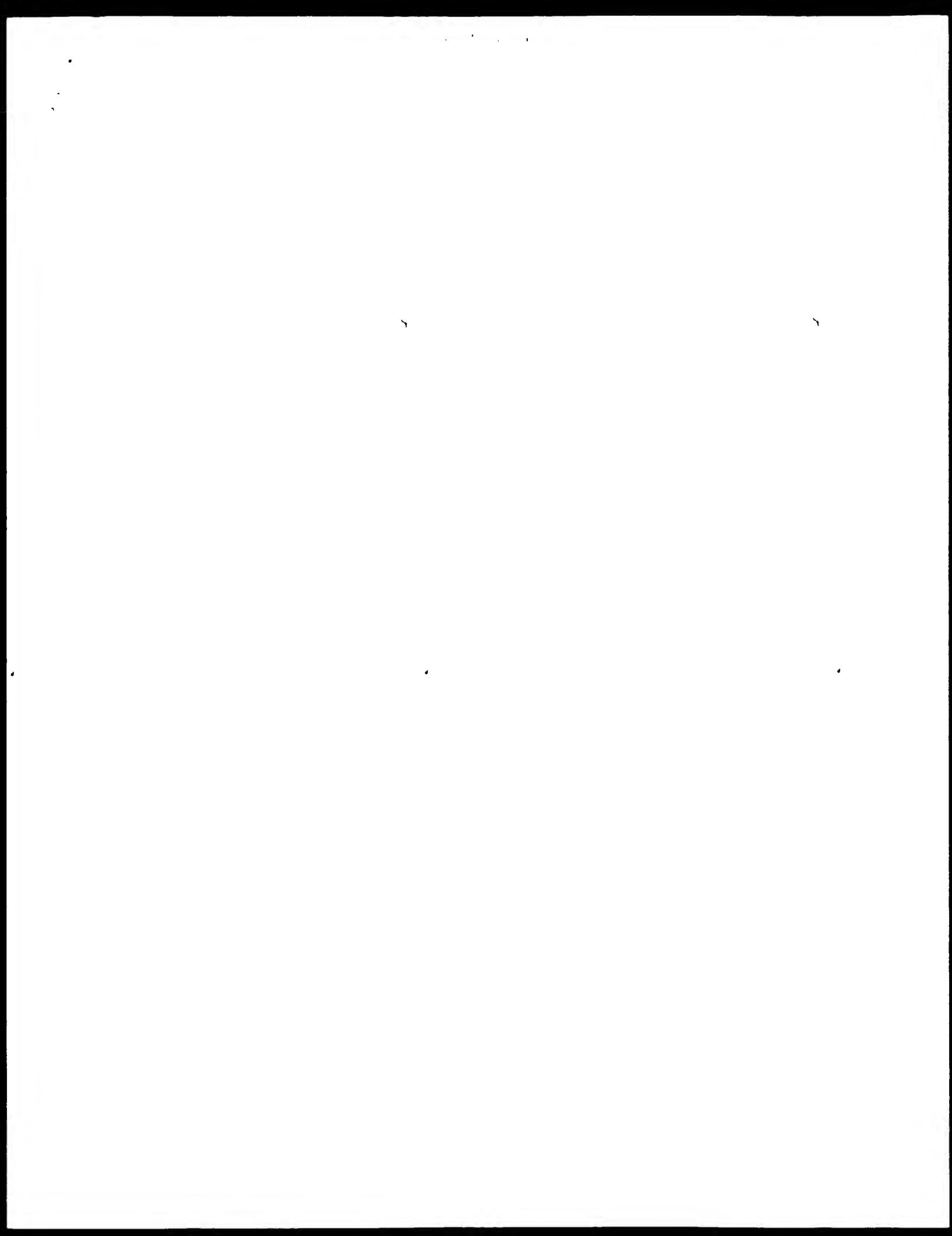
Query Match 12.8%; Score 211; DB 1; Length 364;
 Best Local Similarity 27.1%; Pred. No. 1.2e-09;
 Matches 75; Conservative 50; Mismatches 110; Indels 42; Gaps 10;

Qy 35 PSRSRSPRSVSLQFFNRKPLAGETPRPWVITSGKGVGKTTANGLS 94
 Db 96 PQTQPM-----FTRK-KVPG-VNHIAVSGKGRGKSVTAANLAVLSSQYKVGLID 148
 Qy 95 AGCIGRNLDDLGLENFVNVTVEVINGDGRLDALVRLRKRWSNFELL 154
 Db 149 ADVYGPSPVPTLFGKG-----ERVTVD-QFQTRIPVKEYGLKLSIGFMPMLPSEDPII 200
 Qy 155 FGSKAL-EWLWDLALKTRPE-GSPDRPPIIDCPAGI-DAGF 211
 Db 201 WRCFMLWKLALTEFLFSTKWNGLDFLMDLPPGTDWVITLAQNLVLTGAVVWTFQVAL 260
 Qy 212 RDMDRVTGCLLEDGIDRDKMVLNFRFEMI-----KGEDMMSSVLDWEMI 256
 Db 261 ADVKKAVSM-----PREVNIPVGLVHENMAYFICPSDKKYYVFGKGR-----VAEFANAY 311
 Qy 257 GLSLGIVTPEDSESVRSTNRGPPLVNLKPPILAGLAPEQA 293
 Db 312 GLKLGSIPIDPEVAEKSDFKGEPIVISHPDSEVAKAF 348

Search completed: April 16, 2003, 09:05:24

Job time : 28 secs

RESULT 15
MRP_AQUAE



; Patent No. 6248563

; GENERAL INFORMATION:

; APPLICANT: Ratti, Giulio

; APPLICANT: Comanducci, Maurizio

; APPLICANT: Tecce, Mario F.

; APPLICANT: Giulini, Marzia M.

; TITLE OF INVENTION: pCTD PLASMID ISOLATED FROM CHLAMYDIA

; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY

; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID

; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

; STREET: 301 N. Washington Street

; CITY: Falls Church

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22046-0747

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,544

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/661,820

; FILING DATE: 28-FEB-1991

; APPLICATION NUMBER: IT MI 91A000314

; FILING DATE: 07-FEB-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Svensson, Leonard R.

; REFERENCE/DOCKET NUMBER: 30,330

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-241-1300

; TELEFAX: 703-241-2848

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 264 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-468-544-16

; QUERY MATCH:

; 5.4%; Score 88.5; DB 4; Length 264;

; Best Local Similarity 24.0%; Pred. No. 0.33;

; Matches 53; Conservative 38; Mismatches 76; Indels 107; Gaps 12;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; GENERAL INFORMATION:

; APPLICANT: Kocher, Olivier N.

; TITLE OF INVENTION: pZKL Protein Containing PDZ

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David Prashker, Esq.

; STREET: P.O. Box 67

; CITY: Brookline

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02146

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

; COMPUTER: IBM PS/1

; OPERATING SYSTEM: MS DOS

; SOFTWARE: WordPerfect version 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/997,445D

; FILING DATE: December 23, 1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: David Prashker

; REGISTRATION NUMBER: 29,693

; REFERENCE/DOCKET NUMBER: BJS-037

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 232-7509

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 513 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-997-445D-2

; QUERY MATCH: 5.4%; Score 88.5; DB 3; Length 519; Best Local Similarity 19.3%; Pred. No. 0.33; Matches 53; Conservative 38; Mismatches 76; Indels 107; Gaps 12; Matches 44; Conservative 26; Mismatches 78; Indels 35; Gaps 7;

; QY 32 VNNPNSRNSPIRSVLQPNRKP---ELAEGETPRIVVITSGKGVGKTTTANVGLSLARYGF 88
; DB 212 VQETDRKRVHQKIQKREPAKLPHQPRIVMKKSNG---YGF 255
; QY 89 SVVA-----IDA-----DGLERNLDLGLNENRNYTCVEVINGDRLD--- 127
; DB 256 YLRAGSFOKQIKIKDIDSGPABEAGLKNLVA---VNGESSVETLHDHSVEMTRK 311
; QY 128 ---QALVRDRFWSNFEIJCISKP---PSKPMGFSKAKLWVWAKTKPPEGSDFI 178
; DB 312 GQOTSLVWQKETDNYZRAIFSPFLYVQJWELN-----SVKEAPPTPSL 360
; QY 179 IIDCP-----AGIDAGFTTAITPANEAVLNTPDI 208
; DB 361 EYSSRPTTEVHKPLCRLAKGNGYGFHLNARQGSEFKEVQGGPA---DL 414
; QY 209 TAIRDADRVTLGIECGIRDT---KMTINRVRT 238
; DB 415 AGJEDEDVI---IEVNGVNLVDEPYEKVDRQS 445
; QY 175 -----PDTTIDCPAGIDAGFTTAITPANEAVLNTPDI 222
; DB 107 LKLFINEYCAPFIDCICIDTPPSLGLGLTKEAVFAGDKLIACLTPPEPSLGLQKIREFLS 166
; QY 223 CDG 225
; DB 167 SVG 169
; RESULT 6
; US-09-461-474-6
; Sequence 6: Application US/09461474
; Patent No. 6228042
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Plant Metal Transporters
; FILE REFERENCE: B11303 US NA
; CURRENT APPLICATION NUMBER: US/09/461,474
; EARLIER APPLICATION NUMBER: 60/112,562; RESULT 5
; Sequence 2: Application US/08997445D
; Patent No. 6043342

EARLIER FILING DATE: 1998-12-16
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: Microsoft Office 97
 SEQ ID NO: 6
 LENGTH: 376
 TYPE: PPT
 ORGANISM: *Triticum aestivum*
 US-09-461-474-6

Query Match 5.3%; Score 88; DB 4; Length 376;
 Best Local Similarity 34.0%; Pred. No. 0.22; Mismatches 35; Indels 14; Gaps 5;
 Matches 33; Conservative 15; Mismatches 35; Indels 14; Gaps 5;
 Qy 3 SIRLUSTNHSILPSSLSQKTLISSPRFVNNSPRSPRS--VIGFNRPPELAEETPR 59
 Db 12 SILLFS-RHQ---LRORTL--QPHTRPRMSTAIVSAEADALEPSLQLDORSLR 61
 Qy 60 IWTTSKGAGVKTTTANGLSLARYSWSVILAD 96
 Db 62 WIFV-GKKGAGVKTTTANGLSLARYSWSVILSTD 97

RESULT 7
 PCT-US95-17026-2

Sequence 2, Application PC/TUS9517026

GENERAL INFORMATION:

APPLICANT: ZymoGenetics, Inc.
 APPLICANT: 1201 Eastlake Avenue East
 APPLICANT: Seattle
 APPLICANT: WA

APPLICANT: USA
 APPLICANT: 98102
 TITLE OF INVENTION: Bovine Factor XIII
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc.
 STREET: 1201 Eastlake Avenue East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: PCT-US95/17026

ATTORNEY/AGENT INFORMATION:

FILING DATE: 08-05-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:

NAME: Parker, Gary E

REGISTRATION NUMBER: 31-648

REFERENCE/DOCKET NUMBER: 99-18PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6673
 TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 732 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-17026-2

Query Match 5.3%; Score 88; DB 5; Length 732;
 Best Local Similarity 24.2%; Pred. No. 0.65; Mismatches 38; Indels 94; Gaps 20;
 Matches 72; Conservative 38; Mismatches 94; Indels 94; Gaps 20;

Qy 34 NPSSRSPISVLQFNKPE--LAGETPRIVITSGAGVKTTTANGLSL----- 83
 Db 255 NPKVSRVSGSAM-IWAKDDEGIVLGSWDNVYAY---GVPPSAWTGSVILLEYKSSQK 308

Qy 84 -ARYGFSSWAIDADLGPNLNCI-TLGLENPV. NYTCVEVINGPGRDLD-----QA 129
 Db 309 PVRYGQCKWFE---AGVFNTFLRCIIPAPVWVNTYFAHNDANLQDIFLEEDGNVNSK 364
 Db 150 LIVDKRMSNFEPLICSK--PRSKLPRMGFGKAELFWIIVALKTPPESSPPDFI 11DCPAGI 186
 Qy 365 LTKDSWV-NYH--CNNEAWMTRPDLPGVGG--WQV--VDSTPOENSNDGMYRCGPASV 415
 Db 416 QAIKHHGHCQFQDAPVFA-EVNSDLVY--VIAKCGOHTWAEUDTHIGKLIVTE 469
 Qy 224 --DGIRDIKMVNRVRTDMIK--GEDMMSVLDQEMLG---LSILGVIPEDSEV 270
 Db 470 IGGDGMDI-----TDYKQEGQEEBRLALETAMMYGAKKALNTEGVNLKSKDV 519

RESULT 8

US-08-597-236-5

Sequence 5, Application US/08-97236

Patent No. 573765

GENERAL INFORMATION:

APPLICANT: STINGBLE, Francesca
 APPLICANT: MOLLI, Beat
 TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
 TITLE OF INVENTION: EXOPOLYSACCHARIDES
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Penne & Edmonds
 STREET: 1155 Avenue of the Americans
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/597,236

FILING DATE:

CLASSIFICATION: 426

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95201669.9

FILING DATE: 20-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Fanucci A., Allan

REGISTRATION NUMBER: 30256

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 249 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-597-236-5

Query Match 5.3%; Score 87; DB 1; Length 249;
 Best Local Similarity 20.8%; Pred. No. 0.15; Mismatches 40; Indels 79; Gaps 10;
 Matches 48; Conservative 40; Mismatches 79; Indels 64; Gaps 10;

Qy 41 IRSVLQFNKPE-----LAGETPRIVITSGAGVKTTTANGLSL----- 89
 Db 7 VSKVDFARKTTEVYNTNTQFGAQKMTVAISSEAGEGKSMISVNLASFASVGL 66

Qy 90 VATZDGLRNLGLGLERRVNTIVEVINGDRLQAVRDKRWSIF-----EL 141

Db 67 TLLDAE-TRN----- 105

Qy 142 LG---IS-----YPSKLMGFGKAELFWIIVALKTPPESSPPDFI 185

Db 105 ICPDQISLGLVATASGPVPPNPFLSQ-----NDNFHLMVEARS---CYDVIIDTPVG 157

QY 186 IDAGFITAITPANEAVLVTTPDITALRDPADRVTGL-LCDGIRDIKMIVNRY 236
; Sequence 5, Application US/08746682A
; Patent No. 578684
; GENERAL INFORMATION:
; APPLICANT: STINGELE, Francesca
; APPLICANT: MOLLET, Beat
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
; TITLE OF INVENTION: EXOPOLYSACCHARIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 115 Avenue of the Americans
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,682A
; FILING DATE: 14-NOV-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/597,236
; FILING DATE: 20-JUN-1995
; APPLICATION NUMBER: EP 95-201669.9
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci A., Allan
; REGISTRATION NUMBER: 30256
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-746-682A-5

Query Match 5.3%; Score 87; DB 1; Length 249;
; Best Local Similarity 20.8%; Pred. No. 0.15;
; Matches 48; Conservative 40; Mismatches 79; Indels 64; Gaps 10;

QY 41 IRSVHQFNKPE-----LAKERPRIVITTSCKGGVAKTTTANVQLSLARRYGS 89
; Sequence 41, Application US/08746682A
; Patent No. 578684
; Db 7 VKSXDFAKTTEENYNAIPTNQFSGAQMVKVIAISVEGEKSKMSVNLNTSFAVGLR 66

QY 90 VVAIDADIGLRLNLLGLLGNRNVNTCVENINGDCRQLQALVRDKRWSNF-----EL 141
; Sequence 90, Application US/08746682A
; Patent No. 578684
; Db 67 TLLIDAE--TRN-----SVLSGTFSKNEPY--KGULSFLSGNADLNET 105

QY 142 LC--IS-----KPRSKLPGMFGGKALEWLVDAKTRPFGSPDFIIDC-PAG 185
; Sequence 142, Application US/08746682A
; Patent No. 578684
; Db 106 ICQTDISGLDVIASGPVPPNPTSLQ---NDNFRHMEVARS---CYDVIDTPPG 157

QY 186 IDAGFITAITPANEAVLVTTPDITALRDPADRVTGL-LCDGIRDIKMIVNRY 236
; Sequence 186, Application US/08746682A
; Patent No. 578684
; Db 158 LVIAVIAVIAHQADASLULTEAGKIKRRTVTKAVEQVLQESGSGFLGVNLNKV 208

RESULT 9
; US-08-746-682A-5
; Sequence 5, Application US/08746682A
; Patent No. 578684
; GENERAL INFORMATION:
; APPLICANT: TANG, Li
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: McDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARSONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622-002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Parent In Ver. 2.0
; SEQ ID NO: 18
; LENGTH: 416
; TYPE: PROT
; ORGANISM: Streptomyces venezuelae
; US-09-320-878-18

Query Match 5.2%; Score 86.5; DB 3; Length 416;
; Best Local Similarity 22.2%; Pred. No. 0.39;
; Matches 42; Conservative 31; Mismatches 73; Indels 43; Gaps 7;

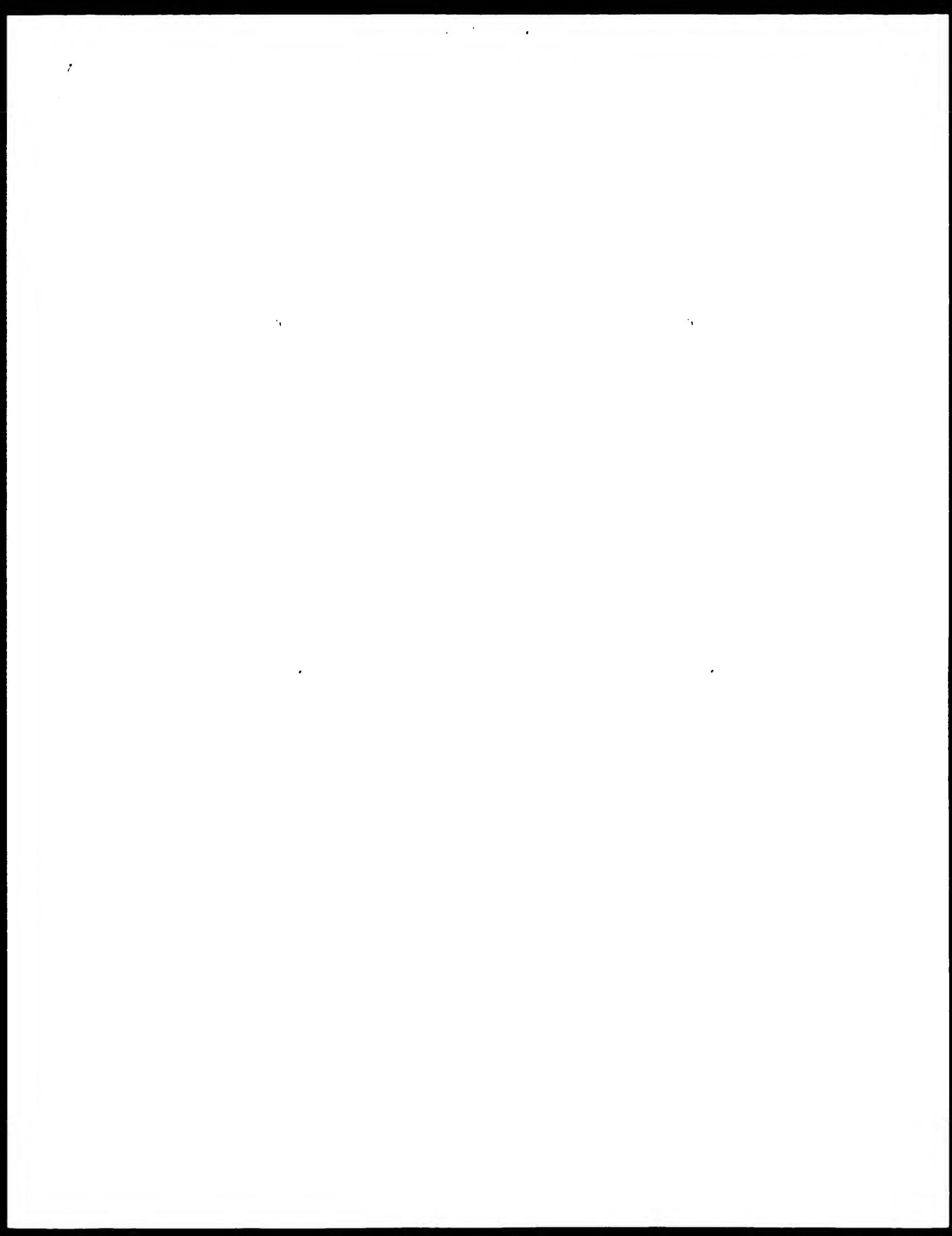
QY 125 RUDQALVFDKWNNSNFFLICLTSKPSRKLPMG3GKALEWLVDALKTRPFGSPDFIIDCPA 184
; Sequence 125, Application US/08746682A
; Patent No. 578684
; Db 102 RURKLVAREFTMRVVEL--RPRVQ-----EIVDGLVNDAMIAAPGRADM----- 145
; Sequence 102, Application US/08746682A
; Patent No. 578684
; QY 185 GIDAGFITAITPANEAVLVTTPDITALRDPADRVTGL-LCDGIRDIKMIV 233
; Sequence 185, Application US/08746682A
; Patent No. 578684
; Db 146 -ESLAWLFLPITVWSELGLGVBPDRAFRAFRVWDAFVFPDDPAQQTAMAEMSGY--LSRLI 202
; Sequence 146, Application US/08746682A
; Patent No. 578684
; QY 234 NRPRTDMIKGEMMSV-----LQVQEMGLSILGVIEPDESEVIRSTRGFLW 282
; Sequence 234, Application US/08746682A
; Patent No. 578684
; Db 203 DSRRGQ--DGEDLSSLALVRLTSDEGSRLTSEELGMIAHILLVAGHETTVNL1ANGMYALL 260
; Sequence 203, Application US/08746682A
; Patent No. 578684
; QY 283 NKEPTLAGL 291
; Sequence 283, Application US/08746682A
; Patent No. 578684
; Db 261 SHPPQLAI 269

RESULT 11
; US-09-105-537-39
; Sequence 39, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sternman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600-438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 39
; LENGTH: 416
; TYPE: PROT
; ORGANISM: Streptomyces venezuelae
; US-09-105-537-39

Query Match 5.2%; Score 86.5; DB 4; Length 416;
; Best Local Similarity 22.2%; Pred. No. 0.39;

RESULT 10
; US-09-320-878-18
; Sequence 18, Application US/09105537A
; Patent No. 611769
; GENERAL INFORMATION:

; Patent No. 5,223,433
 ; APPLICANT: FRANCHINI, GENOVEFFA; WONG-STAALE, FLOSSIE;
 ; GALLO, ROBERT
 ; TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
 ; HUMAN IMMUNODEFICIENCY TYPE 2 PROVIVAL CLONE HIV-2 SBL/ISY
 ; NUMBER OF SEQUENCES: 4
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/331,212
 ; FILING DATE: 03-31-1989
 ; SEQ ID NO.: 2;
 ; LENGTH: 3077
 ; 5223433-2
 ;
 ; Query Match 5.0%; Score 83.5; DB 6; Length 3077;
 ; Best Local Similarity 21.5%; Pred. No. 21; Matches 53; Conservative 30; Mismatches 87; Indels 41; Gaps 14; Matches 61; Gapopen 15; Gaps 15;
 ;
 ; QY 57 TPIWVITSSKGKGKTTTANVGLSARVGFSSVVAIDADLGLI;RNLLLIGLENPVNYYC 115
 ; Db 2037 TPLCYTMNCNASTESAVATTPSGDMINTDPC1QLNNSGGLRBDM--VECOFNMTG 2093
 ; QY 117 VEVINGDCR1DQAI;VPDKPNSNFRLLC--ISKPSKSLPKGFGKAL-----EWLVD 165
 ; Db 2094 LE-----LDKKQYSETWYSKDVCESDNSTKRCYMHNCNTSIVTESCDKHYW-D 2144
 ; QY 166 ALKTRPEGSPDFIILCPAGIDAGFITAIPANEAVLVLTTDPDITALRADDVTCLEDG 225
 ; Db 2145 AMFRYCAAPPGFVLLRCNDNTNSGF---EPNCISKVAST--CIRNMETOPSTWL---G 2194
 ; QY 226 IRDITKIVNVRD---MIKGEDMMSVLDVQEMIGLSILGVIPEDSVWIRST--NRG 277
 ; Db 2195 F-----NCTPAFNHPTYIWHGRDNPITISNKVNLTICRPPENKTVWPITLMSGR 2247
 ; QY 278 F--PLVLUKNKPTLAGLAFEGDQAWRLIVEQDSMKAVVEEBKKG 319
 ; Db 2248 FHSQKNTINPKRQAMCF-F-GSEWPMQF VHQTLV-KHRYKG 2288
 ;
 ; RESULT 15
 ; US-08-416-603-4
 ; Sequence 4, Application US/08416603
 ; Patent No. 5866780
 ; GENERAL INFORMATION:
 ; APPLICANT: Law, Marcus
 ; APPLICANT: Hebara Ledare
 ; APPLICANT: Redick, Bradford B.
 ; TITLE OF INVENTION: Maize Chlorotic Dwarf Virus Genome and
 ; TITLE OF INVENTION: Uses Therefor
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik & Saliwanchik
 ; STREET: 2421 NW 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, version #1.3.0B
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/416,603
 ; FILING DATE: 08-08-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lloyd, Jeffrey
 ; REGISTRATION NUMBER: 35,589
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 904-375-8100
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3457 amino acids



OM protein - protein search, using sw model

Run on: April 16, 2003, 08:59:57 ; Search time: 39 Seconds
(without alignments)

Perfect score: 1674 ; Minimum DB seq length: 0 ; Maximum DB seq length: 200000000
Scoring table: BLOSSUM62 ; Gappen 10.0 , Gapext 0.5 ; Searched: 908470 seqs, 132505620 residues ; Total number of hits satisfying chosen parameters: 908470

Post-processing: Minimum Match: 0% ; Maximum Match: 100% ; Listing first 45 summaries

Database : A_Genseq_101002.*

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2: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1981.DAT.*
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23: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match length	DB ID	%	Summaries
1	1654	100.0	326	21	AAG6531
2	1654	100.0	326	23	AAG77959
3	1654	100.0	343	21	AAG6530
4	1648	99.6	326	21	AAG12922
5	1648	99.6	344	21	AAG12921
6	175.5	71.1	295	23	AAG77960
7	888	53.7	174	21	AAG12923
8	888	53.7	174	21	AAG6532
9	545.5	33.0	266	23	AAG64959
10	365	22.1	260	22	AAB96685

Putative P. abyssi

11	327.5	19.8	245	22	AAB96374	Putative P. abyssi					
12	252.5	15.3	258	22	AAB97119	Putative P. abyssi					
13	224	13.5	294	19	AAY1C920	H. pylori ORF 06p					
14	224	13.5	297	18	AAW20738	H. pylori cytoplas					
15	209	12.6	425	18	AAW20013	H. pylori cytoplas					
16	206	12.5	388	21	AAB11657	A. pylori hypersens					
17	202	12.2	300	22	AAB93146	putative P. abyssi					
18	198	12.0	412	18	AAW20443	H. pylori cytoplas					
19	197.5	11.9	279	22	AAG93171	C glutamicum prote					
20	196.5	11.9	295	22	AAB96518	Putative P. abyssi					
21	191	11.5	390	21	AAG8141	Mycobacterium tube					
22	183	11.1	313	21	AAG11242	Arabidopsis thalia					
23	183	11.1	313	21	AAG43114	Arabidopsis thalia					
24	178	10.8	289	22	AAB34123	Human protein sequ					
25	176	10.6	288	21	AAB93122	Breast and ovarian					
26	173.5	10.5	375	22	AAG90990	C glutamicum prote					
27	171.5	10.4	271	22	AAB95570	Human protein sequ					
28	165	10.0	115	21	AAB4093	Human ORF ORF157					
29	165	10.0	115	23	ABP03821	Human ORF protein					
30	164.5	9.9	478	22	AGG0129	C glutamicum prote					
31	163	9.9	293	22	ABB58550	Drosophila melanog					
32	163	9.9	339	22	AAU39817	Propionibacterium					
33	161	9.7	260	21	AAG71330	Arabidopsis thaliana					
34	161	9.7	400	21	AAG22384	Arabidopsis thaliana					
35	161	9.7	400	21	AAG39877	Arabidopsis thaliana					
36	161	9.7	532	21	AGC2183	Arabidopsis thaliana					
37	161	9.7	532	21	AAG3876	Drosophila melanog					
38	161	9.7	547	21	AAG39875	Arabidopsis thaliana					
39	161	9.7	548	21	AAC2182	Arabidopsis thaliana					
40	159.5	9.6	257	21	AAY75106	Neisseria meningit					
41	158.5	9.6	257	21	AAY75107	Neisseria meningit					
42	157.5	9.5	286	22	ABG96245	Putative P. abyssi					
43	154.5	9.3	350	21	AAG41434	Arabidopsis thalia					
44	152.5	9.2	296	21	AAG41435	Arabidopsis thalia					
45	152	9.2	342	23	ABB47911	Listeria monocytog					
ALIGNMENTS											
RESULT 1											
ID	AAG46531	standard; Protein; 326 AA.									
AC	AAG46531;										
DT	18-OCT-2000	(first entry)									
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 58550.										
XX	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.										
OS	Arabidopsis thaliana.										
XX											
PN	EP1033405-A2.										
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PD	06-SEP-2000.										
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 PR 29-OCT-1999; 9905-0162142.

Query Match 100.0%; Score 1654, DB 21; Length 326;
 best Local Similarity 100.0%; Pred. No. 7.3e-174; Mismatches 0; Indels 0; Gaps 0;
 Matches 326; Conservative 0; Nonsense 0; Insertions 0; PT

Qy 1 MASLRLFSTNHOSLLPPSSLSQKTLISSPRFVNPPSPRSRSPSPSFLVQNPKPLFLAGETPRI 60
 Db 1 MASLRLFSTNHOSLLPPSSLSQKTLISSPRFVNPPSPRSRSPSPSFLVQNPKPLFLAGETPRI 60
 Qy 61 VVITSGKGKVGTTTANGLSLARYGFSVVAIDALRDRVGLLECDGIRDIKMVNRVRTDM 120
 Db 61 VVITSGKGKVGTTTANGLSLARYGFSVVAIDALRDRVGLLECDGIRDIKMVNRVRTDM 120
 Qy 121 NGDCRLQDQALVLRPKWSSNFEELCTSKRSKLMGPGKALEWVDAALKTRPEGSPDFII 180
 Db 121 NGDCRLQDQALVLRPKWSSNFEELCTSKRSKLMGPGKALEWVDAALKTRPEGSPDFII 180
 Qy 181 DCPAGIDAGFITAIPANEAVLVTTPDITALRDRVGLLECDGIRDIKMVNRVRTDM 240
 Db 181 DCPAGIDAGFITAIPANEAVLVTTPDITALRDRVGLLECDGIRDIKMVNRVRTDM 240
 Qy 241 IKGEDMMSVLDVQEMLGSLIGLGVIPEDSEVIRSTNRGFLPVLINKPPTLAGLAFEAQAWRL 300
 Db 241 IKGEDMMSVLDVQEMLGSLIGLGVIPEDSEVIRSTNRGFLPVLINKPPTLAGLAFEAQAWRL 300
 Qy 301 VEQDSMKAQVVEEPKKRGFSFPGG 326
 Db 301 VEQDSMKAQVVEEPKKRGFSFPGG 326

RESULT 2
 AAG77959 standard; Protein; 326 AA.
 AC AAG77959;
 XX DT 01-FEB-2002 (first entry)
 XX DE Arabidopsis thaliana AtMnd1 protein.
 XX KW Mind; AtMind1; chloroplast; plastid; photosynthesis.
 XX OS Arabidopsis thaliana.
 XX PN WO200181601-A2.
 XX PD 01-NOV-2001.
 XX PF 18-APR-2001; 2001WO US12634.
 XX

RESULT 3
 AAG46530
 ID AAG46530 standard; Protein; 343 AA.
 XX AC AAG46530;
 XX DT 18-OCT-2000 (first entry)
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 58549.
 XX KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

PR 19-APR-2000; 2000US-0553431.
 PR XX (UYNE-) UNIV NEVADA & COMMUNITY COLLEGE SYSTEM.
 PR PA
 PR PI Osteryoung KW;
 PR XX DR
 PR XX DR; AAH77248.
 PR PT Novel DNA sequence involved in regulating plastid division in plants characterised by alterations in plastid shape, size and/or number.
 PR PT Example; Fig 1; 35PP; English.
 PR XX CC The sequence represents A. thaliana AtMnd1. The invention relates to a DNA sequence isolated from its native genome comprising a plant Mnd gene that functions in regulating plastid division. When ectopically expressed, the gene alters the number, shape and/or size of chloroplasts and other types of plastids present in plant cells. A genetic construct comprising the gene of the invention in sense or antisense orientation is useful for altering the size, shape and/or number of plastids, in particular chloroplasts in plant cells. Alteration in the plastid size, shape and number improves productivity and increases vigour due to enhanced photosynthetic capacity and allows enhanced production of commercially important compounds that accumulate naturally or as a result of genetic engineering.

SQ Sequence 326 AA;
 PR XX Query Match 100.0%; Score 1654, DB 23; Length 326;
 PR XX Best Local Similarity 100.0%; Pred. No. 7.3e-174; Mismatches 0; Indels 0; Gaps 0;
 PR XX Matches 326; Conservative 0; Nonsense 0; Insertions 0; PT

Qy 1 MASLRLFSTNHOSLLPPSSLSQKTLISSPRFVNPPSPRSRSPSPSFLVQNPKPLFLAGETPRI 60
 Db 1 MASLRLFSTNHOSLLPPSSLSQKTLISSPRFVNPPSPRSRSPSPSFLVQNPKPLFLAGETPRI 60
 Qy 61 VVITSGKGKVGTTTANGLSLARYGFSVVAIDALRDRVGLLECDGIRDIKMVNRVRTDM 120
 Db 61 VVITSGKGKVGTTTANGLSLARYGFSVVAIDALRDRVGLLECDGIRDIKMVNRVRTDM 120
 Qy 121 NGDCRLQDQALVLRPKWSSNFEELCTSKRSKLMGPGKALEWVDAALKTRPEGSPDFII 180
 Db 121 NGDCRLQDQALVLRPKWSSNFEELCTSKRSKLMGPGKALEWVDAALKTRPEGSPDFII 180
 Qy 181 DCPAGIDAGFITAIPANEAVLVTTPDITALRDRVGLLECDGIRDIKMVNRVRTDM 240
 Db 181 DCPAGIDAGFITAIPANEAVLVTTPDITALRDRVGLLECDGIRDIKMVNRVRTDM 240
 Qy 241 IKGEDMMSVLDVQEMLGSLIGLGVIPEDSEVIRSTNRGFLPVLINKPPTLAGLAFEAQAWRL 300
 Db 241 IKGEDMMSVLDVQEMLGSLIGLGVIPEDSEVIRSTNRGFLPVLINKPPTLAGLAFEAQAWRL 300
 Qy 301 VEQDSMKAQVVEEPKKRGFSFPGG 326
 Db 301 VEQDSMKAQVVEEPKKRGFSFPGG 326

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XX
PN
PR 06-SEP-2000.
XX
PR 25-FEB-2000; 2000EP 030:439.
XX
PR 25-FEB-1999; 99JS-012:825.
PR 09-MAR-1999; 99JS-0123548.
PR 23-MAR-1999; 99JS-0123788.
PR 25-MAR-1999; 99JS-0123264.
PR 29-MAR-1999; 99JS-0126785.
PR 01-APR-1999; 99JS-0127462.
PR 05-APR-1999; 99JS-0128234.
PR 08-APR-1999; 99JS-0128714.
PR 16-APR-1999; 99JS-0128845.
PR 19-APR-1999; 99JS-0130077.
PR 21-APR-1999; 99JS-0130449.
PR 23-APR-1999; 99JS-0130510.
PR 28-APR-1999; 99JS-0131144.
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PP 08-MAY-1999; 99JS-0134877.
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PP 07-MAY-1999; 99JS-0134370.
PP 18-MAY-1999; 99JS-0134768.
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PP 20-MAY-1999; 99JS-0135124.
PR 21-JUN-1999; 99JS-0133353.
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PR 27-MAY-1999; 99JS-0136392.
PR 28-MAY-1999; 99JS-0136782.
PR 01-JUN-1999; 99JS-0137223.
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PR 22-JUN-1999; 99JS-0139899.
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PR 30-JUN-1999; 99JS-0141287.
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PR 02-JUL-1999; 99JS-0142055.
PR 06-JUL-1999; 99JS-0142390.
PR 08-JUL-1999; 99JS-0142803.
PR 09-JUL-1999; 99JS-0142950.
PR 12-JUL-1999; 99JS-0142977.
PR 13-JUL-1999; 99JS-0143542.
PR 14-JUL-1999; 99JS-0143624.
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 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161360.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161361.
 PR 26-OCT-1999; 99US-0161373.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161933.
 PR 29-OCT-1999; 99US-0162142.

Query Match 99.6%; Score 1648; DB 21; Length 344;
 Best Local Similarity 99.7%; Pred. No. 3.e-173; Indels 0; Gaps 0;
 Matches 325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASLRLFSTNHOSU, PSSLQSKTLISSPPRUVNNSPSPTRSVI, QFNPKPELAGETPRI 60
 QY 19 MASLRLFSTNHOSU, PSSLQSKTLISSPPRUVNNSPSPTRSVI, QFNPKPELAGETPRI 78
 Db 19 MASLRLFSTNHOSU, PSSLQSKTLISSPPRUVNNSPSPTRSVI, QFNPKPELAGETPRI 78
 QY 61 WITSGKGVGKTTTANVGLSLAPGFSVIAIDQGJPNLILLGLENPVYTCVVI 120
 Db 79 WITSGKGVGKTTTANVGLSLAPGFSVIAIDQGJPNLILLGLENPVYTCVVI 138
 QY 121 NGDRLDOALVDRKRMNPELJ, ISPRSKLPM, 33KALEWVDAKLYKPPESPDFII 140
 Db 199 DCPAGIDAGFITAIPANEAVLWVTPIDITALRDRVIGLJECOGIRDKMVNRVTD 258
 QY 241 IKPDRMMVYDLOQEMGUSLIGVIPDSEVSTNRGEPLVUNKPTAGLAPEQAAMPL 300
 Db 259 IKGDBMMSVLDYQEMLALSLLGVIPDSEVTP, STNP, GFLVNLKEPTLAGLAPEQAAMPL 318
 QY 301 VEQDSMKAVMVVEEPKRGFPSSFGG 326
 Db 319 VEQDSMKAVMVVEEPKRGFPSSFGG 344

RESULT 6
 PR AGT77960
 ID AAG77960 standard; Protein: 295 AA.
 XX AGT77960;
 XX 01-FEB-2002 (first entry)
 DT Tagetes erecta TeMind protein.
 XX KW African marigold; Mind; TeMind; chloroplast; plastid;
 KW photosynthesis.
 OS Tagetes erecta.
 XX FN WO200181601-A2.
 XX PD 01-NOV-2001.
 XX PP 18-APR-2001; 2001WO-US12634.
 XX FR 19-APR-2000; 2000US-0553431.
 PR 19-APR-2000; 2000US-0553431.
 XX (UYNE-) UNIV NEVADA & COMMUNITY COLLEGE SYSTEM.
 XX PI Osterryoung KW;
 XX DR WPI; 2002-041414/05.
 XX N-PSDB; AAH77249.
 XX Novel DNA sequence involved in regulating plastid division in plants
 PT useful for obtaining transgenic plants with novel phenotypes,
 PT characterised by alterations in plastid shape, size and/or number -
 XX Example; Page 34-35; 35pp; English.

The sequence represents *T. erecta* TeMind protein. The invention relates
 CC to a DNA sequence isolated from its native genome comprising a plant
 CC Mind gene that functions in regulating plastid division. When ectopically
 CC expressed, the gene alters the number, shape and/or size of chloroplasts
 CC and other types of plastids present in plant cells. A genetic construct
 CC comprising the gene of the invention in sense or antisense orientation is
 CC useful for altering the size, shape and/or number of plastids, in
 CC particular chloroplasts in plant cells. Alteration in the plastid size,
 CC shape and number improves productivity or increases vigour due to
 CC enhanced photosynthetic capacity and allows enhanced production of

CC commercially important compounds that accumulate naturally or as a result
 CC of genetic engineering.
 XX Sequence 295 AA;

Query: March 71.1%; Score 1175.5, DB 23, Length 295;
 Best Local Similarity 72.0%; Pred. No. 5e-121; Mismatches 15; Gaps 7;
 Matches 247; Conservative 15; Indels 65; Gaps 7;

QY 1 MASLRFLSTNHQLLPLSSISQTKTISSPRVEV-NPSRRS-----PIRSVHQ 45
 Db 1 WTSURF-----LTERSPVCSSTPPIPLHKLTKTPKPKPPRISVQ 47
 QY 47 FNPKPKELAGETPRPIVITSGKGKGKTTTANVGL-SIARYPSVTAIDADGTPNMDLL 106
 Db 48 YNRKPKELAGDTPR-----WAIADAVGLRNNDLL 77
 QY 107 GLENRNYTCVEVINGDRLQALMRDKPMSNFEUCISKPPSKIPMGSGKALELNUA 165
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 78 GLENRNYTCVEVINGDRLQALMRDKPMSNFEUCISKPPSKIPMGSGKALELNUA 136
 QY 167 LKTRPBGSPDTIICPAGIDAGFTAITPANEALVNTPDTAIDADPVTGLRCDGI 226
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 137 LKDRPBGCPDTIICPAGIDAGFTAITPANEALVNTPDTAIDADPVTGLRCDGI 196
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 227 RDIKMIVNVRTUMKGEDMSVLDVQEMGSLTGUPIETS--FVLPSTNPAFPVIVN 283
 Db 197 RDIKMIVNVRTUDLIPGSDMSVLDVQEMGSLI--SDTRGSEFVINSTNRGFFPLVN 252
 QY 284 KPTPLAGLAFEQAAPIVQEDMSKMAVWEEVEEPKXGGFSPFGG 326
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 253 KPPTAGLAFQAAWLVQEDMSKMAVWEEVEEPKXGGFSPFGG 295

RESULT 7

ID AAG12923
 ID AAG12923 standard; Protein; 174 AA.
 AC AAG12923;
 XX DT 17-OCT-2000 (first entry)
 XX DE Arabidopsis thaliana protein fragment SEC ID NO: 12223.
 XX KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 OS Arabidopsis thaliana.
 XX EP1033405-A2.
 PN PD 06-SEP-2000.
 XX PF 25-FEB-2000; 2000EP-0301439
 XX PR 25-FEB-1999; 99US-0128025.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0121548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126364.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 05-APR-1999; 99US-0128334.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0128945.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 23-APR-1999; 99US-0130831.
 PR 28-APR-1999; 99US-0131149.
 PR 30-APR-1999; 99US-0132048.
 PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.
 PR 05-MAY-1999; 99US-012485.
 PR 06-MAY-1999; 99US-0132486.
 PR 06-MAY-1999; 99US-0132487.
 PR 07-MAY-1999; 99US-0132833.
 PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134221.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135253.
 PR 21-MAY-1999; 99US-0135253.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136011.
 PR 27-MAY-1999; 99US-0136592.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137224.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139494.
 PR 18-JUN-1999; 99US-0139495.
 PR 18-JUN-1999; 99US-0139496.
 PR 18-JUN-1999; 99US-0139497.
 PR 18-JUN-1999; 99US-0139498.
 PR 18-JUN-1999; 99US-0139499.
 PR 18-JUN-1999; 99US-0139450.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 21-JUN-1999; 99US-0140917.
 PR 22-JUN-1999; 99US-0139899.
 PR 22-JUN-1999; 99US-0140534.
 PR 23-JUN-1999; 99US-0140554.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140833.
 PR 28-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141877.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-012055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143024.
 PR 14-JUL-1999; 99US-0143232.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 17-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 19-JUL-1999; 99US-0144325.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144834.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145274.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147760.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148219.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148884.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153158.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155339.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0158065.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158332.
 PR 12-OCT-1999; 99US-0158339.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159684.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.

PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 22-OCT-1999; 99US-0160801.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161044.
 PR 25-OCT-1999; 99US-0161405.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161921.
 PR 29-OCT-1999; 99US-0162142.

Query Match 53.7%; Score 888; DB 21; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.3e-89; Mismatches 0; Indels 0; Gaps 0;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 MGFFGKALEWLWALKRPERGSSPPDIIICAGIAGFIAITPANEAVLVTIDPITALR 212
 Db 1 MGFFGKALEWLWALKRPERGSSPPDIIICAGIAGFIAITPANEAVLVTIDPITALR 60

QY 213 DADRVGGLCOCIDPIMVNPVPMIKEDPMVSVLWYEMGSLGIVTIPRSEVIR 272
 Db 61 DADRVGGLCOCIDPIMVNPVPMIKEDPMVSVLWYEMGSLGIVTIPRSEVIR 120

QY 273 STNGFPPLVNLKPTLAGLAAFFQAAWRLVLEDSMFAVMVEEPEPEGEFSEFG 326
 Db 121 STNGFPPLVNLKPTLAGLAAFFQAAWRLVLEDSMFAVMVEEPEPEGEFSEFG 174

RESULT 8

AAG46532
 ID AAG46532 standard, Protein: 174 AA.
 AC AAG46532;
 XX
 DT 18-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 58551.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PR 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123543.
 PR 23-MAR-1999; 99US-01225788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126786.
 PR 01-APR-1999; 99US-01277462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0133449.
 PR 23-APR-1999; 99US-0130510.
 PR 23-APR-1999; 99US-0130891.
 PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.

PR	30-APR-1999;	99US-0132407.	PR	21-JUL-1999;	99US-0145088.
PR	04-MAY-1999;	99US-0132484.	PR	22-JUL-1999;	99US-0145085.
PR	05-MAY-1999;	99US-0132495.	PR	22-JUL-1999;	99US-0145087.
PR	06-MAY-1999;	99US-0132486.	PR	22-JUL-1999;	99US-0145192.
PR	07-MAY-1999;	99US-0132863.	PR	23-JUL-1999;	99US-0145145.
PR	11-MAY-1999;	99US-0134256.	PR	23-JUL-1999;	99US-0145218.
PR	14-MAY-1999;	99US-0134218.	PR	23-JUL-1999;	99US-0145224.
PR	14-MAY-1999;	99US-0134219.	PR	26-JUL-1999;	99US-0145216.
PR	14-MAY-1999;	99US-0134221.	PR	27-JUL-1999;	99US-0145913.
PR	14-MAY-1999;	99US-0134370.	PR	27-JUL-1999;	99US-0145918.
PR	18-MAY-1999;	99US-0134768.	PR	27-JUL-1999;	99US-0145919.
PR	19-MAY-1999;	99US-0134941.	PR	28-JUL-1999;	99US-0145551.
PR	20-MAY-1999;	99US-0135124.	PR	02-AUG-1999;	99US-0145386.
PR	21-MAY-1999;	99US-0135353.	PR	02-AUG-1999;	99US-0146388.
PR	24-MAY-1999;	99US-0135629.	PR	02-AUG-1999;	99US-0146389.
PR	25-MAY-1999;	99US-0136021.	PR	03-AUG-1999;	99US-0145918.
PR	07-JUN-1999;	99US-0137724.	PR	04-AUG-1999;	99US-0147202.
PR	08-JUN-1999;	99US-0138094.	PR	04-AUG-1999;	99US-0147302.
PR	10-JUN-1999;	99US-0138540.	PR	04-AUG-1999;	99US-0147335.
PR	10-JUN-1999;	99US-0138847.	PR	05-AUG-1999;	99US-0147392.
PR	01-JUN-1999;	99US-0137222.	PR	05-AUG-1999;	99US-0148260.
PR	03-JUN-1999;	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	05-JUN-1999;	99US-0137502.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139453.	PR	12-AUG-1999;	99US-0148341.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148365.
PR	18-JUN-1999;	99US-0139454.	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	99US-0139455.	PR	16-AUG-1999;	99US-0147493.
PR	14-JUN-1999;	99US-0139462.	PR	17-AUG-1999;	99US-0149375.
PR	16-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149375.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-014922.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149223.
PR	18-JUN-1999;	99US-0139459.	PR	20-AUG-1999;	99US-0149229.
PR	18-JUN-1999;	99US-0139460.	PR	23-AUG-1999;	99US-0149302.
PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149330.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-0151080.
PR	21-JUN-1999;	99US-0139818.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142055.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155339.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0144086.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142920.	PR	29-SEP-1999;	99US-0156396.
PR	13-JUL-1999;	99US-0142977.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143542.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0143624.	PR	06-OCT-1999;	99US-0157865.
PR	19-JUL-1999;	99US-0144005.	PR	07-OCT-1999;	99US-0158029.
PR	16-JUL-1999;	99US-0144085.	PR	08-OCT-1999;	99US-0158322.
PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.
PR	20-JUL-1999;	99US-0144352.	PR	13-OCT-1999;	99US-0159331.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159337.
PR	21-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159338.
PR	21-JUL-1999;	99US-0144814.	PR	18-OCT-1999;	99US-0159884.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.

Query Match 53.7%; Score 888; DB 21; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.3e-89;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC moncytogenes and related organisms.
 CC Note: The sequence data for this patient did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences.

Db	Sequence	AA;
1	MFGGKAKALEWLVDALKTRPGEPPDFIILDCPAGIDAGFIAITPANEAVLWTPDITALR	60

Qy	121	NGCRLDQALVRKRWNSNELLTSKRSKLMGFGSKALEMLVPAKTRPESGPFFII	180
Db	5	IVITSGKGVGKGTISTANIGTALALQSKVCLIDMDIGLRNIDWVGLENIYDUDV	64
Qy	121	STNRGFPFLVNLNKPTLAIQAFEQRAWPLVEQNSMKAIVVNEEPPKRGFFSFFG	174

DT 05-FEB-2002 (first entry)
 XX
 DE Listeria monocytogenes protein #2163

XX
KW
Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
vitamin B12; bacterial infection; disease;
QY
301 VEQDSKMAVNVEEBFKKGFFS 322

XX
OS
XX
Listeria monocytogenes.

PN WO200177335-A2.
XX
PD 18-QCT-2001.

RESULT 10
AAB6685
ID AAB6685 standard; Protein; 260 AA.

XX 11-APR-2001; 2001WO-FR01118.
XX PF XX
XX AC XX
XX XX AAB96685;

XX 11-APR-2000; 20000PP-00004K29
PA (INSP) INST PASTEUR.
XX 29-OCT-2001 (first entry)
DE Putative P. abyssi ATPase involved in chromosome partitioning #6.

XX
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dussurgey O, Chotouani F, Nedari H, Glaser P, Kunst F, Cossart P;
PI Dujardin C, Nedari H, Glaser P, Kunst F, Cossart P;
XX Hyperthermophilic archaeon; hyperthermophilic protein.

PI Dominguez-Juarez, Goebel, W., Kretz, J., Gunn, M., Ng, E., Vazquez-Boland, J.A., Dominguez-Bernal, G., Garrido-Garcia, P., Tierrez-Martinez, A., Amend, A.; Chakrabarty, T., Domann, E., Hain, T., Berche, C., Charbin, A., Durant, L.; *Pyrococcus abyssi*. OS XX PN FR2192651-A1.

YY	PI	Rechez-Silva, J.	boquerón, García del Portillo, Gómez-López, N.	PI	27-OCT-2000.
YY	PI	Madueno, E.	De Pablo, B.	PD	
YY	PI	Rose, M.	Voss, H.	XX	

DR WPI; 2002-010914/01.
XX. Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment
PT.

PA (CNRS) CNRS CENT NAT RECH SCI. (IFRE-) IFREMER INST FR RECH EXPL MER.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI. (IFRE-) IFREMER INST FR RECH EXPL MER.
 XX
 XX
 PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
 PI Querellou J, Weissenbach J, Saurin W, Heilig R;
 XX
 DR WPI; 2001-126236/14.
 XX
 PT New nucleotide sequences isolated from *Pyrococcus abyssi* encode
 PT proteins useful in industry -
 XX
 PS Claim 7; Pages 1443-1444; 1657pp; French.
 XX
 CC The present invention relates to the genomic sequence of *Pyrococcus*
 CC abyssi (see AAB66431 and AAH41223-7) and *P. abyssi* proteins. *P. abyssi* is
 CC a hyperthermophilic archaeon, which is isolated from deep-sea
 CC hydrothermal vents. The present sequence is one such *P. abyssi* protein.
 CC The proteins of the present invention have various potential industrial
 CC uses, since the proteins are stable at very high temperatures, some up to
 CC 110 degrees centigrade.
 CC Note: This patent is in the same patent family as WO200065062, which
 CC contains additional sequences as shown in AAB99132-AAB99143,
 CC AAH75903-AAH75920 and AAG66436.
 XX
 SQ Sequence 260 AA;
 Query Match 22.1%; Score 366; DB ??; Length 260;
 Best Local Similarity 32.9%; Pred. No. 1.3e-31; Mismatches 88; Indels 50; Gaps 7;
 Matches 94; Conservative 54; Mismatches 88; Indels 50; Gaps 7;
 CC
 QY 59 RIVVITSGKGKVSKTTTANVGLSLARYGFSVATRADLAFNLDLGLGLENRNVNTC 118
 DB 4 RSVIFASGKGKGTTGKTTVANVGLAOFGKVILLADITMANSLILGMD-IVTILHD 62
 QY 119 VINGDFPFLQALVURDKPWSNFELLCSKPRSKLPMR---GKALEWLTALKPREG- 173
 DB 63 VLVGEADLKDKNIYEG-----PASGVKVP3G3LSLEKIRKRAAPRLRDL 104
 QY 174 -----SPDFFIIDCPAGIDAGFITAIPANEAUVLVTDPITALRDAADRVTGLECDGIR 227
 DB 105 IREISOMGDFLIDAPAGLETSITALLIGKELIUTNPEIAITDLSKLVKAELGTI 164
 QY 228 DIKIMINRVPPTDMIKGFDMMVAVLQVFLMGLSISLGVIPPESEVIRSTNTPPFLVNPPT 287
 DB 165 PLGAIALNPTSEKTE---LSPEEIEALLEVPLVGLVPEPEVKAASAYCVPVLLVNPPT 220
 QY 288 LAGLAFBQAA-----WRIVVEQDSMKPAVWVVEEPYKRGFSFEG 325
 DB 221 PAAIAVFFIAVLAGIWFWKPPPEES-----PPVPPITPALFG3 257
 DB 222 GAKAFVKLQAEVFLAGKA 241
 RESULT 11
 AAB96374 ID AAB96374 standard; Protein; 245 AA.
 XX
 AC AAB96374;
 XX
 AAB96374; 29-OCT-2001 (first entry)
 DE Putative *P. abyssi* ATPase involved in chromosome partitioning #3.
 XX
 KW Hyperthermophilic archaeon; hyperthermophilic protein.
 XX
 OS Pyrococcus abyssi.
 PN FR2792651-A1.
 XX
 PD 27-OCT-2000.
 XX
 PR 21-APR-1999; 99FR-0005034.
 XX
 PR 21-APR-1999; 99FR-0005034.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI. (IFRE-) IFREMER INST FR RECH EXPL MER.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI. (IFRE-) IFREMER INST FR RECH EXPL MER.
 XX
 PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
 PI Querellou J, Weissenbach J, Saurin W, Heilig R;
 XX
 DR WPI; 2001-126236/14.
 XX
 PT New nucleotide sequences isolated from *Pyrococcus abyssi* encode
 PT proteins useful in industry -
 XX
 PS Claim 7; Pages 1058-1059; 1657pp; French.
 XX
 CC The present invention relates to the genomic sequence of *Pyrococcus*
 CC abyssi (see AAB66431 and AAH41223-7) and *P. abyssi* proteins. *P. abyssi* is
 CC a hyperthermophilic archaeon, which is isolated from deep-sea
 CC hydrothermal vents. The present sequence is one such *P. abyssi* protein.
 CC The proteins of the present invention have various potential industrial
 CC uses, since the proteins are stable at very high temperatures, some up to
 CC 110 degrees centigrade.
 CC Note: This patent is in the same patent family as WO200065062, which
 CC contains additional sequences as shown in AAB99132-AAB99143,
 CC AAH75903-AAH75920 and AAG66436.
 XX
 SQ Sequence 245 AA;
 Query Match 19.8%; Score 327.5; DB 22; Length 245;
 Best Local Similarity 34.6%; Pred. No. 2.1e-27; Mismatches 90; Indels 31; Gaps 8;
 Matches 90; Conservative 49; Mismatches 90; Indels 31; Gaps 8;
 CC
 QY 59 RIVVITSGKGKVSKTTTANVGLSLARYGFSVATRADLAFNLDLGLGLENRNVNTC 118
 DB 3 RISIVSGKGKGTTGKTTVANVGLAOFGKVILLADITMANSLILGMD-IVTILHD 61
 QY 119 VINGDFPFLQALVURDKPWSNFELLCSKPRSKLPMR---GKALEWLTALKPREG- 173
 DB 62 VLVGEADLKDKNIYEG-----PASGVKVP3G3LSLEKIRKRAAPRLRDL 104
 QY 170 RPEGSPPFIIDCPAGIDAGFITAIPANEAUVLVTDPITALRDAADRVTGLECDGIR 229
 DB 110 --GDDYFLIDAPAGLQDAMSAMSSEEALEVNTPEISCTDTMKVGIURKAGLAI 166
 QY 230 FMTVNRV.RTDMIKGFDMMVAVLQVFLMGLSISLGVIPPESEVIRSTNTPPFLVNPPT 288
 DB 167 GFLINRGRTENDIPPA---AQDMVDFLIAVIEDPAREGTLEGIAPAVKYKESE 221
 QY 289 AGLAFQAMWLVVEQDSMKPAVWVVEEPYKRGFSFEG 309
 DB 222 GAKAFVKLQAEVFLAGKA 241
 RESULT 12
 AAB96719 ID AAB96719 standard; Protein; 258 AA.
 XX
 AC AAB96719;
 XX
 AAB96719; 29-OCT-2001 (first entry)
 DE Putative *P. abyssi* ATPase involved in chromosome partitioning #7.
 XX
 KW Hyperthermophilic archaeon; hyperthermophilic protein.
 XX
 OS Pyrococcus abyssi.
 PN FR2792651-A1.
 XX
 PD 27-OCT-2000.
 XX
 PR 21-APR-1999; 99FR-0005034.
 XX
 PR 21-APR-1999; 99FR-0005034.
 XX

PD 19-DEC-1996. KW
 XX 96WO-US09122.
 PF 06-JUN-1996; XX
 XX 96US-0630405.
 PR 01-APR-1996; OS
 PR 07-JUN-1995; XX
 XX 95US-0487032.
 PA (ASTR) ASTR A B.
 PA
 PI Berglindh OT, Smith D, Mellgaard BL;
 XX DR
 DR WPI; 1997-052306/05.
 XX N-PSDB; AAT6791.
 PT Helicobacter pylori nucleic acid sequences and related
 PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
 PT infection, and to detect Helicobacter
 PS Claim 61; Page 115; 1481pp; English.
 XX
 CC The present sequence is a Helicobacter pylori cytoplasmic protein
 CC The protein may be used in a vaccine to prevent or treat H. pylori
 CC infection or to identify H. pylori polypeptide binding compounds,
 CC useful as potential H. pylori life cycle activators or inhibitors,
 CC The genomic sequence of H. pylori (ATCC 55679) was determined from
 CC overlapping contigs generated by mechanically shearing the bacterial
 CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
 CC and the predicted coding regions defined by computer evaluation. To
 CC identify likely H. pylori antigens for vaccine development, the amino
 CC acid sequences predicted from various ORF were analysed for significant
 CC homology to other known or exported membrane proteins. Having identified
 CC and determined the sequences of interest, particular regions can be
 CC isolated from H. pylori by PCR amplification for recombinant polypeptide
 CC production, e.g. in E. coli hosts.
 SQ Sequence 297 AA;
 Query Match 13.5%; Score 224; DB 18; Length 297;
 Best Local Similarity 29.1%; Pred. No. 8e-16;
 Matches 87; Conservative 40; Mismatches 106; Indels 66; Gaps 11;
 CC
 Qy 55 GETPRRIWITSGKGCGVKITTTANVGSLARYGFSVVAIDADGLRNLLIGLENRVN 114
 Db 28 GNT-KFIAITSGKGCGVKITTTANVGSLARYGFSVVAIDADGLRNLLIGLENRVN- 85
 Qy 115 TCEVINGVCRDQALVRDKRWSNPFELICISKRSKPLMG-----FGKALEWLV 164
 Db 86 -ILHALKGBAQQ-----EICIEBGLCLPGDSGBELKLYVSGAEDALDRFV 132
 Qy 165 DALKRTRPEG---SPDFIILIDCPAGIDAGFITAIPANEAVLUTPDTIALRDAWRVGLL 221
 Db 133 D-----EEGVLLSLYDVIDTGAGIGATQAOBNASDCVWVITTPBPSAITDA-----Y 181
 Qy 222 ECDGCR-----DIIKIVRVA-----RTDMIKR-----MSVLDVQEMI-----GSLISLGVIP 265
 Db 182 ACTIKNSKNDDELFLIANNQCPKREGATYERPLFKVAKNNTS-----LELHVIGATE 234
 Qy 266 EDSEVIRSTNRGFLPLVINKPPTLAGLFQEQAMPLVQFQNSMKAWMFEEPKPGCFSSFF 324
 Db 235 NSSLILKRYVERKLRKIAPNLDFLFSQSTDQIASLILVKLETGL-----EIPKEGKSF 289
 SQ Sequence 425 AA;
 Query Match 12.6%; Score 209. DB 18; Length: 425;
 Best Local Similarity 24.2%; Pred. No. 6.4e-14;
 Matches 86; Conservative 57; Mismatches 112; Indels 82; Gaps 12;
 CC
 Qy 8 STMHQSLPLPSLSQKTLISSPRLSSPRFVNNPSRSPSPRSVLPQNPKE-----LAGETPR 59
 Db 105 SSBETSAILRENNISKAMCQEKGVKALNDIYTPP-----RTQAPKPTTNAKNNIH 155
 Qy 60 IVITSSKGKVKITTTANVGSLARYGFSVVAIDADGLRNLLIGLENRVNVTCEV 119
 Db 156 VNMISCKGGVGSKTSPTSVNLSIAJANLNQKVGLDADYGPNTFRMMGLQ----- 205
 Qy 120 TMDCRD-----QALVTDKRSNPFELICISPPSPLPMPF---GGKALEWLVALKTRPE 172
 Db 206 -NAEVIMDPSGKKL-----FLKAFC-----VSMVSMGLYDEGOSLIWRGMLMRAIEQ 254
 Qy 173 -----GSPFPIIDCPAGIDAGFIT-----AIPANEAVLUTPDTIALRDA----- 216
 Db 255 MLDSDIWGDDLVWVDMPPGTDQTLAQAVPLSAGITVTTPOVSLDDAKRSLDMPFK 314
 Qy 217 ... VIGCLE ... -CGGDRDMEVIVHVRPMINGEDMMSSLDVQEMGLSLIGVPE 266
 Db 315 LHPPIAGIVENMGFSVCEHCK-----KESIFGNSMSGL--LBAYNTQILAKPL 363
 Qy 267 DSEVIRSTNRGFLPLVINKPPTLAGLFQEQAMPLVQFQNSMKAWMFEEPKPGCFSSFF 297
 Db 364 EPKVKPLGGDKGEPPIVSHPSVSAKIFEMW 394

KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
 KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
 XX
 OS Helicobacter pylori.
 PN WO640893-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96US-0630405.
 XX
 PR 01-APR-1996; 96WO-US09122.
 XX
 PR 07-JUN-1995; 95US-0487032.
 XX
 PA (ASTR) ASTR A B.
 PA
 PI Berglindh OT, Smith D, Mellgaard BL;
 XX DR
 DR WPI; 1997-052306/05.
 XX N-PSDB; AAT68266.
 PT Helicobacter pylori nucleic acid sequences and related
 PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
 PT infection, and to detect Helicobacter
 PS Claim 61; Page 1402-1403; 1481pp; English.
 XX
 CC The present sequence is a Helicobacter pylori cytoplasmic protein.
 CC The protein may be used in a vaccine to prevent or treat H. pylori
 CC infection or to identify H. pylori polypeptide binding compounds, useful
 CC as potential H. pylori life cycle activators or inhibitors. The genomic
 CC sequence of H. pylori (ATCC 55679) was determined from overlapping
 CC contigs generated by mechanically shearing the bacterial DNA. The
 CC sequences were analysed for ORF of at least 180 nucleotides, and the
 CC predicted coding regions defined by computer evaluation. To identify
 CC likely H. pylori antigens for vaccine development, the amino acid
 CC sequences predicted from various ORF were analysed for significant
 CC homology to other known or exported membrane proteins. Having identified
 CC and determined the sequences of interest, particular regions can be
 CC isolated from H. pylori by PCR amplification for recombinant polypeptide
 CC production, e.g. in E. coli hosts.
 SQ Sequence 425 AA;
 Query Match 12.6%; Score 209. DB 18; Length: 425;
 Best Local Similarity 24.2%; Pred. No. 6.4e-14;
 Matches 86; Conservative 57; Mismatches 112; Indels 82; Gaps 12;
 CC
 Qy 8 STMHQSLPLPSLSQKTLISSPRLSSPRFVNNPSRSPSPRSVLPQNPKE-----LAGETPR 59
 Db 105 SSBETSAILRENNISKAMCQEKGVKALNDIYTPP-----RTQAPKPTTNAKNNIH 155
 Qy 60 IVITSSKGKVKITTTANVGSLARYGFSVVAIDADGLRNLLIGLENRVNVTCEV 119
 Db 156 VNMISCKGGVGSKTSPTSVNLSIAJANLNQKVGLDADYGPNTFRMMGLQ----- 205
 Qy 120 TMDCRD-----QALVTDKRSNPFELICISPPSPLPMPF---GGKALEWLVALKTRPE 172
 Db 206 -NAEVIMDPSGKKL-----FLKAFC-----VSMVSMGLYDEGOSLIWRGMLMRAIEQ 254
 Qy 173 -----GSPFPIIDCPAGIDAGFIT-----AIPANEAVLUTPDTIALRDA----- 216
 Db 255 MLDSDIWGDDLVWVDMPPGTDQTLAQAVPLSAGITVTTPOVSLDDAKRSLDMPFK 314
 Qy 217 ... VIGCLE ... -CGGDRDMEVIVHVRPMINGEDMMSSLDVQEMGLSLIGVPE 266
 Db 315 LHPPIAGIVENMGFSVCEHCK-----KESIFGNSMSGL--LBAYNTQILAKPL 363
 Qy 267 DSEVIRSTNRGFLPLVINKPPTLAGLFQEQAMPLVQFQNSMKAWMFEEPKPGCFSSFF 297
 Db 364 EPKVKPLGGDKGEPPIVSHPSVSAKIFEMW 394

KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;
 KW

RESULT 15
 AAW21013
 ID AAW21013 standard; protein; 425 AA.
 XX
 AC AAW21013;
 XX
 DT 22-JUL-1997 (first entry)
 DE H. pylori cytoplasmic protein, hp5e1521lorf13.
 KW

Thu Apr 17 10:30:02 2003

usb-10-067-989-1.rag

Page 16

Search completed: April 16, 2003, 09:06:09
Job time : 41 secs

Gencore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 09:04:32 ; Search time 45 Seconds
 (without alignments)
 69.6.440 Million cell updates/sec

Title: IIS-10-067-989-1
 Perfect score: 1654
 Sequence: 1 MASLRLFSTNHOSLLPSSL... KAVVVEEEPKPKPGRFSPFEGG 326

Scoring table:

BioSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR 73; *
 1: Piri: *
 2: pir2: *
 3: pir3: *
 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query

Match length DB ID

Description

Result No.	Score	Query	Match length	DB ID	Description
1	792	47.9	282	2 T07303	cell division inhibitor - Chlorella vulgaris chloroplast
2	657.5	39.8	268	3 A12237	septum site-determ hypothetical prote
3	643.9	38.9	266	2 AB2270	septum site-determ
4	573.5	34.7	276	2 D75478	septum site-determ
5	559.5	33.8	263	2 B97054	cell division inhibitor - Chlorella vulgaris chloroplast
6	546.5	33.0	266	2 AB1330	hypothetical prote
7	545.5	33.0	266	2 AHI1267	septum site-determ
8	536.5	32.4	264	2 CB4697	cell division inhibitor - Chlorella vulgaris chloroplast
9	522.6	31.6	1	1 G45239	hypothetical prote
10	516.5	31.2	262	2 P70375	hypothetical prote
11	514.5	31.1	269	2 C82695	hypothetical prote
12	506.5	30.6	268	2 C64561	hypothetical prote
13	500.5	30.3	268	2 B71945	hypothetical prote
14	487.9	29.4	270	2 AE0253	hypothetical prote
15	483.2	29.2	270	2 AH0724	hypothetical prote
16	481.5	29.1	271	2 C98327	hypothetical prote
17	481.5	29.1	271	2 AB2200	hypothetical prote
18	480.5	29.1	271	2 F82329	hypothetical prote
19	479.0	29.0	270	1 CCCTD	hypothetical prote
20	479.0	29.0	270	2 E90837	hypothetical prote
21	479.0	29.0	270	2 F85695	hypothetical prote
22	475.5	28.7	271	2 A72200	hypothetical prote
23	468.2	28.3	276	2 C82136	hypothetical prote
24	460.2	27.8	270	2 B84968	hypothetical prote
25	452.3	27.3	271	2 A96C11	hypothetical prote
26	449.5	27.2	271	2 C81230	hypothetical prote
27	398.2	23.5	245	2 AB3625	hypothetical prote
28	366.2	22.1	260	2 F75175	hypothetical prote
29	344.5	22.0	259	2 B69113	hypothetical prote

ALIGNMENTS

RESULT 1
 T07303
 cell division inhibitor - Chlorella vulgaris chloroplast
 C;Species: chloroplast Chlorella vulgaris
 C;Date: 14-May-1999 #sequence_revision 14-May-1999 #Text_change 21-Jul-2000
 R;Iwakagi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, S.; Tsuzuki, J.; Nakash; Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
 A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo; A;Reference number: Z15985, NCID:9703241; PMID:159184
 A;Accession: T07303
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-282 <WAT>
 A;Cross-references: EMBL:AB01684; NID:3222452; PID:BA57951; 1; P12322467
 A;Genetics:
 A;Gene: mind
 A;Name: chloroplast
 C;Superfamily: cell division inhibitor mind
 C;Keywords: chloroplast

Query Match 47.9%; Score 792; DB 2; Length 282;
 Best Local Similarity 60.4%; Pred. No. 5e-56; Gaps 5;
 Matches 165; Conservative 39; Mismatches 55; Indels 14; Gaps 5;

QY 59 RIWVITSGKGGVKTITANVGLSARYGFSVATDADGLRNIDLLGLENNRNYTCVE 118
 Db 17 RVIWITSGKGGVKTITANVGLSARYGFSVATDADGLRNIDLLGLENNRNYTCVE 118
 AB465.5 33.8 263 2 B97054
 AB1330 33.0 266 2 AHI1267
 CB4697 32.4 264 2 C84697
 G45239 31.6 1 G45239
 P70375 31.2 262 2 P70375
 C82695 31.1 269 2 C82695
 C64561 30.6 268 2 C64561
 B71945 30.3 268 2 B71945
 AE0253 29.4 270 2 AE0253
 AH0724 29.2 270 2 AH0724
 C98327 29.1 271 2 C98327
 AB2200 29.1 271 2 AB2200
 F82329 29.1 271 2 F82329
 CCCTD 29.0 270 1 CCCTD
 E90837 29.0 270 2 E90837
 F85695 29.0 270 2 F85695
 A72200 28.7 271 2 A72200
 C82136 28.3 276 2 C82136
 B84968 27.8 270 2 B84968
 A96C11 27.3 271 2 A96C11
 C81230 27.2 271 2 C81230
 AB3625 23.5 245 2 AB3625
 F75175 22.1 260 2 F75175
 B69113 22.0 259 2 B69113

RESULT 2
 A12237
 septum site-determining protein [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp.
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #Text_change 30-Jun-2002

Query Match 33.8%; Score 559.5; DB 2; Length 263;
 Best Local Similarity 44.7%; Pred. No. 2e-37; Indels 11; Gaps 4;
 Matches 117; Conservative 57; Mismatches 77; Indels 11; Gaps 4;
 C;Species: Listeria innocua

Qy 61 WVTSGKGKGKGGKTTTANVGLSLARRYGFSVVAIDADLGLRNLDLGLLENRNYTCVVI 120
 Db 5 IVITSGKGKGKGGKTTTANVGLSLARRYGFSVVAIDADLGLRNLDLGLLENRNYTCVVI 64

Qy 121 NGCPLDQALVDPDKWMSNFEELGCKSPSKLPLMFGGKALEWLVDAKTRPEGSPPDFII 180
 Db 65 EGNCNLQKLTKDHYENALLPQTQPKNDV--KPKQMLKVNLYKE--EEFYVII 118

Qy 181 DCPAGIDAGFITAATPANEAVLVTTPDITALRDAVRTGVLGLCDDGIRDKIMIVNRRTDM 240
 Db 119 DCPAGIDAGFITAATPANEAVLVTTPDITALRDAVRTGVLGLCDDGIRDKIMIVNRRTDM 240

Qy 241 IKGENMSVLDQEMGLSLGIVIPEDSEVIRSTNRGFLPLVNPPLAGLAFEQAWRL 300
 Db 179 VPKGKGIGFIVNIVNLAIRLIGVWVNPDKOITVSTNKGEPILVNQNAN-AGKAFRDARRV 237

Qy 301 VEQDSMKAVMVEEPKRGFFS 322
 Db 238 LGEE---VPFEKYETQGRIA 255

RESULT 6

AB1630
 Cell division inhibitor (septum placement) protein Mind homolog mind [imported] - Listeria innocua
 C;Species: Listeria innocua
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 C;Accession: AB1630
 R;Gisler, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Science 294, 849-852, 2001
 A;Authors: Krest, J.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Makrilia, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID: 21537279; PMID: 11679669
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-266 <GLA>
 A;Cross-references: GR-003210; PMID:NC_004622.1; PMID:91641077; GSFRB; GN00177
 A;Experimental source: strain BGD-e
 C;Genetics:
 A;Gene: mind
 C;Superfamily: cell division inhibitor mind

Query Match 33.0%; Score 545.5; DB 2; Length 266;
 Best Local Similarity 43.9%; Pred. No. 2.6e-36; Indels 9; Gaps 5;
 Matches 115; Conservative 59; Mismatches 79; Indels 9; Gaps 5;
 C;Species: Listeria innocua

Qy 61 WVTSGKGKGKGGKTTTANVGLSLARRYGFSVVAIDADLGLRNLDLGLLENRNYTCVVI 120
 Db 5 IVITSGKGKGKGGKTTTANVGLSLARRYGFSVVAIDADLGLRNLDLGLLENRNYTCVVI 64

Qy 121 NGCPLDQALVDPDKWMSNFEELGCKSPSKLPLMFGGKALEWLVDAKTRPEGSPPDFII 180
 Db 65 FGCKWHDAMIKPFDL-LFLPAACTTWNAVSGBWMLNQL--RPD-YDFII 119

Qy 181 DCPAGIDAGFITAATPANEAVLVTTPDITALRDAVRTGVLGLCDDGIRDKIMIVNRRTDM 240
 Db 120 DCPAGIDAGFITAATPANEAVLVTTPDITALRDAVRTGVLGLCDDGIRDKIMIVNRRTDM 240

Qy 241 IKGENMSVLDQEMGLSLGIVIPEDSEVIRSTNRGFLPLVNPPLAGLAFEQAWRL 300
 Db 180 MMQPMWQDIDETTTHSTELGIGITDCEVIECISGDDVAM-LPNTTAAQGFIARRI 238

Qy 301 VEQDSMKAVMVEEPKRGFFS 322
 Db 239 LGEE---SIPLMSTETKKGAGFFA 257

RESULT 8

C84028
 Septum site-determining protein mind [imported] - *Bacillus halodurans* (strain C-125)
 C;Species: *Bacillus halodurans*
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C;Accession: C84028
 R;Tokami, H.; Nakase, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirano, N.; Nucleic Acids Res 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its comparative genomics
 A;Reference number: AB3650; MUID: 20512582; PMID:11058132
 A;Status: preliminary
 A;Molecule type: DNA

A; Residues: 1-264 <STO>
 A; Cross-references: GB:PP001517; GB:BA000004; NID:910175500; PIDN:BA06746.1; GSPDB:GN0C
 A; Experimental source: strain C 125
 C; Genetics:
 A; Gene: mind
 C; Superfamily: cell division inhibitor mind
 Query Match Similarity 32.4%; Score 536.5; DB 2; Length 264;
 Best Local Similarity 41.1%; Pred. No. 1.4e-35; Matches 109; Conservative 66; Mismatches 83; Indels 7; Gaps 3;
 Db 61 WITSGKGGKGKTTTANGLSLARYGSVVAADDAGIURNLIGLENRNPY"CEV1 120
 Db 5 IVITSGKGGKGKTTTANGLSLARYGSVVAADDAGIURNLIGLENRNPY"CEV1 120
 Qy 121 NGDRDQALVDRKWSNFELLCTSKPSKSLPKPFGSKALEWLVDAALKTRPEGSPPDFII 180
 Db 65 EGRRLRQALKDRFECMNLPAQTKR-SAVTEQMKRIVEELQ---EFDVII 118
 Qy 181 DCPGAGDAGPITAATPANEAVLVTDPITALRDAVDRLGLEDGIRDIMKVNPRPTD 240
 Db 119 DCPAGIEQFKNAYAGADRAVADRLIGLEKEVEAPLIVNIRGHM 178
 Qy 241 IKGEDMMSVLUQOMGLSLIGVLPEDSEVIRNGLPVLKPPLAGAFEQAWRL 300
 Db 179 MKNGMDLVDEIVSIALIELGIVDDEVKFSNKGEPIALH-FPSKASYAVRNIAARI 237
 Qy 301 VEQDSMKAQVWEEPKRKGFSPPG 325
 Db 238 LGETVPLMSFEQEVKVLAKIKSPPG 262

RESULT 9

G45239
 cell division inhibitor mind [validated] - *Bacillus subtilis*
 C; Species: *Bacillus subtilis*
 C; Accession: 10-Jun-1993 #sequence revision 04-Oct-1995 #text change 19-Jan-2001
 R; Lee, S.; Price, C.W.
 Mol. Microbiol. 7, 601-610, 1993
 A; Title: The minCD locus of *Bacillus subtilis* lacks the minE determinant that provides t
 A; Reference number: S3104; MUID:9321302; PMID:8459776
 A; Accession: S312nc
 A; Molecule type: DNA
 A; Residues: 1-268 <LEF>
 P; Levin, P.A.; Marcollis, P.S.; Seelow, R.; Losick, R.; Sun, D.
 J. Bacteriol. 174, 6717-6728, 1992
 A; Title: Identification of *Bacillus subtilis* genes for septum placement and shape determ
 A; Preference number: A45239; MUID:93015731; PMID:1400224
 A; Status: not compared with conceptual translation
 A; Molecule type: DNA
 A; Residues: 1-268 <LEF>
 A; Cross-references: GB:MG0343; NID:9142852; PIDN:AAA22401.1; PID:9142859
 A; Note: sequence extracted from NCBI backbone (NCBIP:116563)
 R; Varley, A.W.; Stewart, G.C.
 J; Bacteriol. 174, 6729-6742, 1992
 A; Title: The divIVB region of the *Bacillus subtilis* chromosome encodes homologs of Esche
 A; Preference number: A45440; MUID:93015732; PMID:1400225

RESULT 10

F7Q375
 cell division inhibitor (septum placement) mind2 - *Aquifex aeolicus*
 C; Species: *Aquifex aeolicus*
 C; Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 26-Aug-1999
 C; Accession: F70375
 F; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
 V; Nature 392, 353-358, 1998
 A; Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
 A; Reference number: A70300; MUID:98196666; PMID:9537320
 A; Accession: F70375
 A; Molecule type: DNA
 A; Residues: 1-262 <AQF>
 A; Cross-references: GB:AE000712; NID:92983411; PID:37981413; GP:AFN0655;
 A; Experimental source: strain VFS5
 C; Genetics:
 A; Gene: mind2
 C; Superfamily: cell division inhibitor mind
 Query Match Similarity 31.2%; Score 516; DB 2; Length 262;
 Best Local Similarity 41.4%; Pred. No. 6e-34;

A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, Y.; Ogawa, K.; Ogawa, A.; Oudaga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, A.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadzic, V.; Satoh, T.; Scanlon, A.; Schleicher, S.; Schroeter, F.; Scuffene, F.; Sekiguchi, J.; Sokowska, A.; Seror, Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. A; Reference number: A69580; MUID:98044033; PMID:9384377
 A; Accession: A69580
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-268 <KUN>
 A; Cross-references: GB:Z99118; GB:AL009126; NID:92635200; PIDN:CA014753.1; PID:32635264
 A; Experimental source: strain 168
 C; Genetics:
 A; Gene: mind
 A; Start codon: TGG
 C; Function:
 A; Description: mediates, together with minC, cell division site selection by specifically
 C; Superfamily: cell division inhibitor mind
 C; Keywords: cell division control; nucleotide binding; P-loop
 F; 0-17/Region: nucleotide-binding motif A (P-loop)
 F; 16/Binding site: ATP (Lys) #Status Predicted
 Query Match Similarity 31.6%; Score 523; DB 1; Length 268;
 Best Local Similarity 41.1%; Pred. No. 1.7e-34; Matches 111; Conservative 68; Mismatches 77; Indels 14; Gaps 7;
 Db 61 WITSGKGGKGKTTTANGLSLARYGSVVAADDAGIURNLIGLENRNPY"CEV1 120
 Db 5 IVITSGKGGKGKTTTANGLSLARYGSVVAADDAGIURNLIGLENRNPY"CEV1 120
 Qy 121 NGDRDQALVDRKWSNFELLCTSKPSKSLPKPFGSKALEWLVDAALKTRPEGSPPDFII 180
 Db 65 EGRRLRQALKDRFECMNLPAQTKR-SAVTEQMKRIVEELQ---EFDVII 118
 Qy 181 DCPGAGDAGPITAATPANEAVLVTDPITALRDAVDRLGLEDGIRDIMKVNPRPTD 240
 Db 119 DCPAGIEQFKNAYAGADRAVADRLIGLEKEVEAPLIVNIRGHM 178
 Qy 241 IKGEDMMSVLUQOMGLSLIGVLPEDSEVIRNGLPVLKPPLAGAFEQAWRL 300
 Db 179 MKNGMDLVDEIVSIALIELGIVDDEVKFSNKGEPIALH-FPSKASYAVRNIAARI 237
 Qy 301 VEQDSMKAQVWEEPKRKGFSPPG 325
 Db 238 LGETVPLMSFEQEVKVLAKIKSPPG 262

A;Reference number: A71800; MVID: 99129557; PMID: 9923582
 A;Accession: B1945
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-268 <APN>
 A;Cross-references: GB:AE00148; SR:AE00149; MVID: 34154938; PID: AAC05905_1; PID: 9415485
 A;Genetics:
 C;Genetics: mind
 C;Superfamily: cell division inhibitor mind

Query Match 30.3%; Score 500.5; DB 2; Length 268;

Best Local Similarity 39.8%; Pred. No. 1.1e-32; Matches 109; Conservative 65; Mismatches 81; Indels 19; Gaps 5;

QY 60 IIVVITSGKGKGGVKTITANVGLSLARYGFSVVAIDAPIGLRNLDDLGLENRNYTCVE 119
 Db 4 WVTITSGKGKGGVKTSSAATGAGQKKTWIDFDIGLRNLDDLGCRVVFDFN 63

QY 120 IIVGPRIDALVURKWRKRSWFLCISPKSKLPMGFGGGKALEWLWALKTRPEGSPDFI 179
 Db 64 MFKNKNLSQLITPEKTEKFLSFLMASQSKDNPNIILDKEVAT--LNLAR - ADFDYL 117

QY 180 IDCAGIDAGFITTATPANEAVLWTPITALADRVTGLEGIR:... - DIKMI 232
 Db 118 IDSPAGIESGFHEAHLHADMALWVTPVEVSSLRSDRVIGITDAKSNRAKSGEEVHKHLI 177

QY 233 VNPVPTOMTKGEDMSVLDQVGMGLSLGNVPEDESEVIRSINGPFLVNLNPFTAGLA 292
 Db 178 INRKPFLVANGEMTIEVVKLICLPRIGPRPHHISANKEVIL - PTDESAKA 235

QY 293 FEOQAWRLVQEQDSKMAVWEEPEPKRGRPSFFCG 326
 Db 236 YQPTTPRIDGEE---VEVVEFKNKGPGPSALKG 265

RESULT 14
 AE0253
 C;Species: Yersinia pestis (strain CG92)
 C;Accession: AE0253
 C;Accession: AE0253
 R;Parkhill, J.; Wren, B. W.; Thomson, N. R.; Titball, R. W.; Holden, M. T. G.; Prentice, M. B.; Chillingworth, T.; Cronin, A.; Davies, P. M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AE0001; MVID: 2147413; PMID: 1186360
 A;Accession: AE0253
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-270 <KRP>
 A;Cross-references: GB:AL51338C; PID: CAD05498_1; PID: 31560302; SR:SPR 3400176
 C;Genetics:
 C;Genetics: mind
 C;Superfamily: cell division inhibitor mind

Query Match 29.3%; Score 483; DB 2; Length 270;
 Best Local Similarity 41.2%; Pred. No. 2.8e-31; Matches 114; Conservative 57; Mismatches 88; Indels 18; Gaps 8;

QY 59 RIVVITSGKGKGGVKTITANVGLSLARYGFSVVAIDAPIGLRNLDDLGLENRNYTCVE 119
 Db 3 RIVVITSGKGKGGVKTSSAATGAGQKKTWIDFDIGLRNLDDLGCRVVFDFN 62

QY 119 VNGCDRQALVDRKWSNFLLCISPKSKLPMGFGGGKALEWLWALKTRPEGSPDFI 178
 Db 63 VQCDATINQAIKIDPTENIFFLAPSPQDPAITRPEVAK VLDLSYAM--DEFI 117

QY 179 IIMPAJIDAGFITTATPANEAVLWVTPDITALADRVTGLEGIR:... - DEFI 230
 Db 118 VCDSPAGIETGALMAYFADAEITAINTPEVSSVRSDSFILGILASKSPFAENKEEPIKEY 177

QY 231 MIVNVRDMDIGEDMSVLDQVGMGLSLGNVPEDESEVIRSINGPFLVNLNPFTAG 290
 Db 178 LLLTRYNPGVRKGDMMSLMEVLEIURIKLVGVPEDQSVLRAASNOQEPVILAD-AQ 236

QY 232 LAFEGAAWRLVQEQDSKMAVWEEPEPKRGRPSFFCG 326
 Db 237 KAYADTVPLGEE-PPPFEEEE--KKGFLPLFGG 270

Search completed: April 16, 2003, 09:08:36

Job time : 46 secs

QY 231 MIVNVRDMDIGEDMSVLDQVGMGLSLGNVPEDESEVIRSINGPFLVNLNPFTAG 290
 Db 178 LLLTRYNPGVRKGDMMSLMEVLEIURIKLVGVPEDQSVLRAASNOQEPVILAD-AQ 236
 QY 291 LAFEGAAWRLVQEQDSKMAVWEEPEPKRGRPSFFCG 326
 Db 237 KAYADTVPLGEE-PPPFEEEE--KKGFLPLFGG 270

RESULT 15
 AH0724
 C;Sepium site determining protein [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi
 A;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A;Note: this species has also been called *Salmonella typhi*
 C;Accession: AH0724
 C;Accession: AH0724
 R;Parkhill, J.; Dougan, G.; James, K. D.; Thomson, N. R.; Pickard, D.; Wain, J.; Churcher, S.; Moulle, S.; O'Gara, P.
 Nature 413, 848-852, 2001
 A;Authors: Parkhill, J.; Wain, K.; Fotheringham, M.; Simmonds, M.; Skellam, J.; Stevens, R.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi
 A;Reference number: AB0502; PMID: 11677608
 A;Accession: AH0724
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-270 <PAR>
 A;Cross-references: GB:AL51338C; PID: CAD05498_1; PID: 31560302; SR:SPR 3400176
 C;Genetics:
 C;Genetics: mind
 C;Superfamily: cell division inhibitor mind

Query Match 29.3%; Score 483; DB 2; Length 270;

Best Local Similarity 41.2%; Pred. No. 2.8e-31; Matches 114; Conservative 57; Mismatches 88; Indels 18; Gaps 8;

QY 59 RIVVITSGKGKGGVKTITANVGLSLARYGFSVVAIDAPIGLRNLDDLGLENRNYTCVE 119
 Db 3 RIVVITSGKGKGGVKTSSAATGAGQKKTWIDFDIGLRNLDDLGCRVVFDFN 62

QY 119 VNGCDRQALVDRKWSNFLLCISPKSKLPMGFGGGKALEWLWALKTRPEGSPDFI 178
 Db 63 VQCDATINQAIKIDPTENIFFLAPSPQDPAITRPEVAK VLDLSYAM--DEFI 117

QY 179 IIMPAJIDAGFITTATPANEAVLWVTPDITALADRVTGLEGIR:... - DEFI 230
 Db 118 VCDSPAGIETGALMAYFADAEITAINTPEVSSVRSDSFILGILASKSPFAENKEEPIKEY 177

QY 231 MIVNVRDMDIGEDMSVLDQVGMGLSLGNVPEDESEVIRSINGPFLVNLNPFTAG 290
 Db 178 LLLTRYNPGVRKGDMMSLMEVLEIURIKLVGVPEDQSVLRAASNOQEPVILAD-AQ 236

QY 232 LAFEGAAWRLVQEQDSKMAVWEEPEPKRGRPSFFCG 326
 Db 237 KAYADTVPLGEE-PPPFEEEE--KKGFLPLFGG 270

Search completed: April 16, 2003, 09:08:36

Job time : 46 secs

QY 59 RIVVITSGKGKGGVKTITANVGLSLARYGFSVVAIDAPIGLRNLDDLGLENRNYTCVE 119
 Db 3 RIVVITSGKGKGGVKTSSAATGAGQKKTWIDFDIGLRNLDDLGCRVVFDFN 62

QY 119 VNGCDRQALVDRKWSNFLLCISPKSKLPMGFGGGKALEWLWALKTRPEGSPDFI 178
 Db 63 VQCDATINQAIKIDPTENIFFLAPSPQDPAITRPEVAK VLDLSYAM--DEFI 117

QY 179 IIMPAJIDAGFITTATPANEAVLWVTPDITALADRVTGLEGIR:... - DEFI 230
 Db 118 VCDSPAGIETGALMAYFADAEITAINTPEVSSVRSDSFILGILASKSPFAENKEEPIKEY 177

QY 231 MIVNVRDMDIGEDMSVLDQVGMGLSLGNVPEDESEVIRSINGPFLVNLNPFTAG 290
 Db 178 LLLTRYNPGVRKGDMMSLMEVLEIURIKLVGVPEDQSVLRAASNOQEPVILAD-AQ 236

QY 232 LAFEGAAWRLVQEQDSKMAVWEEPEPKRGRPSFFCG 326
 Db 237 KAYADTVPLGEE-PPPFEEEE--KKGFLPLFGG 270

Search completed: April 16, 2003, 09:08:36

Job time : 46 secs

QY 1 MASLRLFSTNHQSILIPSSLSQKTLISPRFVNNPSSRSPRSVSLQFNRPKPELAGERTPRI 60
Db 1 MASLRLFSTNHQSILIPSSLSQKTLISPRFVNNPSSRSPRSVSLQFNRPKPELAGERTPRI 60
QY 61 WITSGKGGVCKTTTANYGLSLARYGFSWAIDADGLRNLNLLGLENRNYTVEVI 120
Db 61 WITSGKGGVCKTTTANYGLSLARYGFSWAIDADGLRNLNLLGLENRNYTVEVI 120
QY 121 NGDCUDQALVRDKWSNELLCSKPSKLPKMGFFGKALEWLVDAKTRPESPPFII 180
Db 121 NGDCUDQALVRDKWSNELLCSKPSKLPKMGFFGKALEWLVDAKTRPESPPFII 180
QY 181 DCPAGIDAGFITAATPANAVLVTPTDITALRDPVAGLCKDGRDIDMVNVRPTDM 240
Db 181 DCPAGIDAGFITAATPANAVLVTPTDITALRDPVAGLCKDGRDIDMVNVRPTDM 240
QY 241 IKGEDMSVLDVQEMGSLLLGVFEDSVIRSTRNGFPLVANKRPLLAGLAFQAWRL 300
Db 241 IKGEDMSVLDVQEMGSLLLGVFEDSVIRSTRNGFPLVANKRPLLAGLAFQAWRL 300
QY 301 VEQDSMKAVVNEEVEPKKRGFPSSFGG 326
Db 301 VEQDSMKAVVNEEVEPKKRGFPSSFGG 326

RESULT 2

Q9FV40 PRELIMINARY; PRT; 295 AA.
ID Q9FV40
AC Q9FV40;
DT 01-MAR-2001 (TREMBrel 16, Created)
DT 01-MAR-2002 (TREMBrel 20, Last annotation update)
DE Mind.
OS Tagetes erecta (African marigold).
OC Spermatozoa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Asteridae; eudicots; core eudicots;
OC Helianeae; Tagetes.
OX NCBI_TaxID:13708;
RN [1]
RP SEQUENCE FROM N A
RC STRAIN=CV; NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (G3)" genomic DNA, chromosome 6, PAC
clone:PP044B06.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP001129; BAA90628.1;
DR InterPro; IPR000707; AIPase_Para.
DR Pfam; PF00991; Para; 1.
SQ SEQUENCE 306 AA; 32341 MW; CECAB382195:2690 CRC64;

Query Match 64.5%; Score 607.5; DB 10; Length 306;
Best Local Similarity 68.4%; Pred. No. 9.7e-80; DB 10;
Matches 216; Conservative 31; Mismatches 5C; Indels 19; Gaps 5;
OC 14 JIUPSSLSQKTLISPRFVNNPSSRSPIRVLFQFVPLKPELAGERTPRIWITSGKGGVCKT 73
Db 7 LLLPS-----RCPPASSPAPHG-----RTAPELSGPTPRVUVUTS3KGVGKT 51

QY 74 TTANGLSLARYGFSWAIDADGLRNLNLLGLENRNYTVEVIWINGCRDQALVRD 133
Db 52 TTANLAASLNLTSLSAWAVADAGRNLLGLENRNYTVEVIWINGCRDQALVRD 111
QY 134 KRWSNFELCISKPSKLPKMGFFGKALEWLVDAKTRPESPPFIIIDCPAGIDAGFITA 193
Db 113 RAHDGCLCISKPSKLPKMGFFGKALEWLVDAKTRPESPPFIIIDCPAGIDAGFITA 170
QY 194 ITPANEAVLVTPTDITALRDPVAGLCKDGRDIDMVNVRPTDMIKGEDMSVLDVQ 253
Db 171 IAPFEEAVLVTPTDITALRDPVAGLCKDGRDIDMVNVRPTDMIKGEDMSVLDVQ 230
QY 254 EMIGLSLIGVIFEDSEVIRSTRNGFPLVANKRPLLAGLAFQAWRLVEODSMKAVVNEE 313
Db 231 EMIGLSLIGVIFEDSEVIRSTRNGFPLVANKRPLLAGLAFQAWRLVEODSMKAVVNEE 290
QY 314 E - PKR-GFESFFGG 326
Db 291 QERPKKKAGFFSSFGG 306

RESULT 3

Q9LWY6 PRELIMINARY; PRT; 306 AA.
ID Q9LWY6
AC Q9LWY6;
DT 01-OCT-2000 (TREMBrel 15, Created)
DT 01-OCT-2000 (TREMBrel 15, Last sequence update)
DE Similar to Chlorella vulgaris C-27 chloroplast DNA.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatozoa; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartidae; Oryzeae; Oryza.
OX NCBI_TaxID:4530;
RN [1]
RP SEQUENCE FROM N A
RC STRAIN=CV; NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (G3)" genomic DNA, chromosome 6, PAC
clone:PP044B06.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP001129; BAA90628.1;
DR InterPro; IPR000707; AIPase_Para.
DR Pfam; PF00991; Para; 1.
SQ SEQUENCE 306 AA; 32341 MW; CECAB382195:2690 CRC64;

Query Match 64.5%; Score 607.5; DB 10; Length 306;
Best Local Similarity 68.4%; Pred. No. 9.7e-80; DB 10;
Matches 216; Conservative 31; Mismatches 5C; Indels 19; Gaps 5;
OC 14 JIUPSSLSQKTLISPRFVNNPSSRSPIRVLFQFVPLKPELAGERTPRIWITSGKGGVCKT 73
Db 7 LLLPS-----RCPPASSPAPHG-----RTAPELSGPTPRVUVUTS3KGVGKT 51

QY 74 TTANGLSLARYGFSWAIDADGLRNLNLLGLENRNYTVEVIWINGCRDQALVRD 133
Db 52 TTANLAASLNLTSLSAWAVADAGRNLLGLENRNYTVEVIWINGCRDQALVRD 111
QY 134 KRWSNFELCISKPSKLPKMGFFGKALEWLVDAKTRPESPPFIIIDCPAGIDAGFITA 193
Db 113 RAHDGCLCISKPSKLPKMGFFGKALEWLVDAKTRPESPPFIIIDCPAGIDAGFITA 170
QY 194 ITPANEAVLVTPTDITALRDPVAGLCKDGRDIDMVNVRPTDMIKGEDMSVLDVQ 253
Db 171 IAPFEEAVLVTPTDITALRDPVAGLCKDGRDIDMVNVRPTDMIKGEDMSVLDVQ 230
QY 254 EMIGLSLIGVIFEDSEVIRSTRNGFPLVANKRPLLAGLAFQAWRLVEODSMKAVVNEE 313
Db 231 EMIGLSLIGVIFEDSEVIRSTRNGFPLVANKRPLLAGLAFQAWRLVEODSMKAVVNEE 290
QY 314 E - PKR-GFESFFGG 326
Db 291 QERPKKKAGFFSSFGG 306

RESULT 4

Q9TP6 PRELIMINARY; PRT; 274 AA.
ID Q9TP6
AC Q9TP6;
DT 01-MAY-2000 (TREMBrel 13, Created)
DT 01-MAY-2000 (TREMBrel 13, Last sequence update)
DE Sequester-site determining protein.
GN MND.
OS Nephroselms olivacea.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendrales; Chlorodendraceae; Nephroselms.

QY 107 GLENNSVNYTVEVINGCPDQALVRDKWSNELLCSKPSKLPKMGFFGKALEWLVDA 166
Db 78 GLENNSVNYTVEVINGCPDQALVRDKWSNELLCSKPSKLPKMGFFGKALEWLVDA 136
QY 167 LKTRREGSPFLIDCPAGIDAGFITAATPANAVLVTPTDITALRDPVAGLCKDGRDII 226
Db 137 LKDRQEGCPDFILDCPAGIDAGFITAATPANAVLVTPTDITALRDPVAGLCKDGRDII 196
QY 227 RDIKMTVNRVRTDMIKGEDMSVLDVQEMGSLLLGVFEDSVIRSTRNGFPLVLN 283
Db 197 RDIKMTVNRVRTDMIKGEDMSVLDVQEMGSLLLGVFEDSVIRSTRNGFPLVLN 252

OX NCBI_TaxID=31312;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=93398634; PubMed=10468594;
 RA Turmel M.; Otis C.; Lemieux C.;
 RT "The complete chloroplast DNA sequence of the green alga *Nephroselmis*
 olivacea: Insights into the architecture of ancestral chloroplast
 genomes." Proc. Natl. Acad. Sci. U.S.A. 90:10248-10253 (1993).
 RN [2] SEQUENCE FROM N.A.
 RA Turmel M.; Otis C.; Lemieux C.;
 RL Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF107379; AAD49081; -;
 DR AF107379; AAD54881; -;
 DR InterPro; IPR000707; ATPase_Para.
 DR Pfam; PF00991; Para; 1.
 KW Chloroplast
 SQ SEQUENCE 274 AA; 30126 MW; 9D0A1449E6815845 CRC64;
 Query Match 45.7%; Score 756; DB 8; Length 274;
 Best Local Similarity 58.7%; Pred No. 3; 46-54;
 Matches 155; Conservative 39; Mismatches 60; Indels 10; Gaps 3;
 QY 59 RIVVITSGKGCGVGKTTTANGLSLARYGFSVVAIDATUGLERNLLEGLLENRYTCVE 118
 DB 14 RIVVITSGKGCGVGKTTTANGLSLARYGFSVVAIDATUGLERNLLEGLLENRYTCVE 73
 QY 119 VINGCRLDOALVRKRKRSWNSFELICISKPKSLPQGKALEWLVDAIKTRPREGSPDFI 178
 DB 74 VIEGQCRLEQALIPKPKWQHLSLAMISKFRQYNN-TPRMMIMIVDSTKEP--GYQYI 12A
 QY 179 IIDCAGIDAGFITAATPANEAVLVTTPDITALDADPVTGILFGDGIPDIDKMLVNRPYI 238
 DB 129 LIDCPAGIDAGFVNIAAPADEALITYPELTAIRDADRVAGLLEANDFVNRLVANRPYI 188
 - QY 239 DM1KQGDDMMSVLVDQEMIGLSLGVIPEDSEVIRSTNRQFPLVNLKPPPLAGLAFEQAW 298
 - 189 EMIQDNMMSVVDQVGMGIPULGAIPEDKVNITSNRGEPLYCOKTITLAGVAFEEAR 248
 - Db 299 RLVEEDSMKAVMVEEPEPKRGFFS 322
 - Db 249 RLVGLPS---PSDAPSRGWFA 267
 RESULT 5
 ID Q9TR6 PRELIMINARY; PRT; 359 AA.
 AC 09TR6; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE Septum site-determining Protein.
 GN MND OR ALR456.
 OS *Anabaena* sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=2195283; PubMed=11759840,
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kimura T.,
 RA Watanabe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohira M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium *Anabaena* sp. strain PCC 7120.";
 RL DNA Res. 8:205-213 (2001);
 DR EMBL; AP003593; BAB5155.1; -;
 DR InterPro; IPR000707; ATPase_Para.
 DR Pfam; PF00991; Para; 1.
 DR Complete proteome.
 SQ SEQUENCE 268 AA; 39262 MW; 02C4A9D604C1CBCC CRC64;
 Query Match 39.8%; Score 657.5; DB 16; Length 268;
 Best Local Similarity 54.4%; Pred. No. 4.1e-46;
 Matches 137; Conservative 48; Mismatches 54; Indels 13; Gaps 4;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=263-11;
 RA Krauf U.; Hachtel W.;
 OC Eukaryota; Viridiplanteae; Chlorophyta; Trebouxiophyceae; Chlorellales;
 OC Chlorellaceae; Prototrichaceae.
 OX NCBI_TaxID=3111;
 DR Cell division inhibitor Mind.
 DE Cell division inhibitor Mind.
 GN MIND.
 OS Prototrichaceae.
 OC Chloroplast
 OC Chloroplast
 OC Chloroplast
 RT "A 22 kb fragment of the 53 kb plastid genome of the colourless alga
 "Prototrichaceae" *wickerhamii* containing *atp-*, *rpl-*, *rps-*, *rnr-*, and *trn-*
 genes." Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AJ45645; CAB53105.1; -;
 DR InterPro; IPR000707; ATPase_Para.
 DR Pfam; PF00991; Para; 1.
 KW Chloroplast
 SQ SEQUENCE 359 AA; 40804 MW; B550EAF50BC0A51E CRC64;

RP SEQUENCE FROM N.A.
 RC STRAIN=NR4T / JCM1007;
 RX MEDLINE=C1193816; PubMed=1199736;
 RA Bao Q., Tian Y., Li W., Xu Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of *T. tengcongensis* genome.;"
 PI Genome Res. 12:689-700(2002);
 DR EMBL; AE01307; RMM24159.1; -.
 KW Complete proteome.
 SQ SEQUENCE 264 AA; 29357 MW; 3F85B51D77C6859C CRC64;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=2188634; PubMed=11899109;
 RA Kapratchayya A., Bartman I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhatrachayya A., Gardner W., Grecchin G., Zhu L.,
 RA Vasiera O., Chu L., Kogan Y., Chata O., Gotsman E., Bernai A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fornstein M., Kyrpides N., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium *Fusobacterium* nucleatum strain ATCC 25586.;"
 RT nucleatum strain ATCC 25586.;"
 PI J. Bacteriol. 184:9018-9022.
 DR EMBL; AE010531; AAL94382.1; -.
 KW Complete proteome.
 SQ SEQUENCE 264 AA; 28675 MW; DA74D05DF8ED1F68 CRC64;
 Query Match 36.7%; Score 574.5; DB 16; Length 264;
 Best Local Similarity 50.0%; Pred. No. 6.3e-42;
 Matches 121; Conservative 55; Mismatches 59; Indels 7; Gaps 3;
 Query 59 RIVVUTSGKGCGVKTITANGLSLARYFSVVAIDGLRLNLDLGLGLENRVNYTCVE 118
 Db 4 RVIWVTSKGKGCGVKTITANGLAGLADKGHKVVLIDTIGLRLNLDVNGLENRVYDVLV 63
 Query 119 VNGDPRIPDGLVPRKPSWFEELGTSKSPSKLPMGFCOKALEWLVALKTRPREGPDFI 178
 Db 64 VIEERPRISAFKIKHKGCPNLVLLPAQIDPNDV-TPEQMSLSDSLK---ASFDYI 117
 Query 179 IIDCPAGIDAGFTTAITPANEAVVJVTIDTALRDRDVTGLECDGIRDKIMVNRV 238
 Db 118 IVDCPAGIEQCGFKNAVADEAVVVTTPESVATRDRDVTGLEASIGKPERPLVNLKI 177
 Query 239 DMKGEDMMMSVLDVOEMLGISLGQVIPERSEVIRSTNGPFLVNLKPTTLAGIAFQAAW 298
 Db 178 DMVKDNMLSVEDDILGKLGVPDDETIVSINKGEPPLVY-KGDSLAANKAFKNIAN 236
 RESULT 8
 OC Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococaceae; Deinococcus.
 OC NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R;
 RX STRAIN=R;
 RX MEDLINE=20016896; PubMed=10567266;
 RA white O., Eisen J. A., Heidelberg J. F., Hickey E. K., Peterson J. D.,
 RA Dodson R. J., Haft D. H., Gwinn M. L., Nelson W. C., Richardson D. L.,
 RA Moffat K. S., Qin H., Jiang L., Pamphilis W., Crosby M., Shou M.,
 RA Vamathevan J. J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K. S., Aravind L., Daly M. J., Minton K. W., Fleischmann R. D.,
 RA Ketchum K. A., Nelson K. E., Salzberg S., Smith H. O., Venter J. C.,
 RA Fraser C. M.;
 RT "Genome sequence of the radioresistant bacterium *Deinococcus* radiodurans R1;"
 RT radiodurans R1;"
 RL Science 286:1571-1577(1999);
 EMBL; AE001931; AAH10331.1; -.
 DR TIGR; DR0752; -.
 DR InterPro; IPR000707; ATPase PatA.
 DR InterPro; IPR000392; NitrogenaseII.
 DR Pfam; PF00142; fer4_NIFH; 1.
 DR Pfam; PF00991; RrA; 1.
 KW Complete proteome.
 SQ SEQUENCE 276 AA; 29420 MW; AD74FDCF45920D9C CRC64,
 [1]
 ID Q8RRB9 PRELIMINARY; PRT; 264 AA.
 AC Q8RRB9;
 AC 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Septum formation inhibitor-activating ATPase.
 DE MIND OR TMB0903.
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Bacilli; Clostridia; Clostridiaceae;
 OC Thermanaerobacteriales; Thermanaerobacteriaceae; Thermanaerobacter.
 OC NCBI_TaxID=119072;
 RN [1]

Query Match 34.7%; Score 573; DB 16; length 276.
 Best Local Similarity 44.3%; Pred No 3.5e-39;
 Matches 125; Conservative 52; Mismatches 72; Indels 33; Gaps 5;

QY 59 RIVVITSGKGKGVKTTTANVGLSLARYGFSVVAIDADGLNLDDLLGLENRNVTCVE 118
 Db 12 KVIVVITSGKGKGVKTTTANVGLSLARYGFSVVAIDADGLNLDDLLGLENRNVTCVE 118
 QY 119 VINGCPRIDALVDEKWMWNFELICISPRSKLPMGKGAKLGEKVWIDVUGLRLNDVNGLESRVVFDLV 71
 Db 72 VLEGKCRMNQALIRKDRVNLHLLPASOTDK-----DALDDEPEVKEVWKG 117
 QY 171 --PESSPDFIIIDEPAGIDAGFTITAITANEAIVLWTPDITALRDAADVTRGCGIRD 228
 Db 118 LLEEEGFDFRLDIDPAGIESGRMAAPREGALVWNPVEVSVRDAADRIGLEAQITE 177
 QY 229 IWTINPVPITMVKSEDMMSVLDVZEMGLSLSLGVIPDESEVIRSTRGFLVNLKPTL 288
 Db 178 IRLVNRKPKVNAWSGNMISDDKWDLIGVKGPKGFFS---FFGG 326
 QY 289 AGLAEQAWLVEGDSMAGAAMVPEEPKKGFFS---FFGG 326
 Db 236 AGDAFMATQPIQGQVPPKLFER---KGTMWAIIRPLFGG 274

RESULT 10

Q8X111 PRELIMINARY; PRT; 265 AA.
 AC Q8X111; 01-MAR-2002 (TREMBrel. 20, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Septum site-determining protein Mind, Atpase.
 GN CAC249
 OS Clostridium acetobutylicum
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787,
 RX MEDLINE:2139325; PubMed:11466286,
 RA Nöelting J., Breton G., Omelchenko, M. V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Oiu D., Hitti J., Wolf Y.I., Daly M.J., Tatusov R.L., Salatino P., Doucette-Stamm L., Soucaille P., Soucaille P., Bennett G.N., Koonin E.V., Smith D.R.,
 RT "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838 (2001).
 DR EMBL, AAB07638; AAC7221.1;
 DR InterPro; IPR000707; Atpase_Para.
 DR Pfam; PF00991; Para; 1.
 KW Complete proteome.
 SQ SEQUENCE 263 AA; 28769 MW; B06AFBEA9DCF3D73 CRC64;

Query Match 33.8%; Score 559; DB 16; length 263;
 Best Local Similarity 44.7%; Pred No. 4.6e-38;
 Matches 117; Conservative 57; Mismatches 77; Indels 11; Gaps 4;

QY 61 VVITSGKGKGVKTTTANVGLSLARYGFSVVAIDADGLNLDDLLGLENRNVTCVEI 120
 Db 5 IVITSGKGKGVKTTTANVGLSLARYGFSVVAIDADGLNLDDLLGLENRNVTCVEI 120
 QY 121 NGCRLQALVDEKWMWNFELICISPRSKLPMGKGAKLGEKVWIDVUGLRLNDVNGLESRVVFDLV 64
 Db 65 EGCRKLQALIKRKHVNLALIPTAQITRDKNV--KPECMUKLNUELKE---EFDVYI 118
 QY 181 DCAGIDAGFTITAITANEAIVLWTPDITALRDAADVTRGCGIRDKIMVNRTM 240
 Db 119 DCAGIDAGFTITAITANEAIVLWTPDITALRDAADVTRGCGIRDKIMVNRTM 240
 QY 241 IKGEDMSVLDVZEMGLSLSLGVIPDESEVIRSTRGFLVNLKPTL 300
 Db 179 DCAGIDAGFTITAITANEAIVLWTPDITALRDAADVTRGCGIRDKIMVNRTM 237
 RESULT 12

Q92BHO ID Q92BHO PRELIMINARY, PRT, 265 AA.
 AC Q92BHO;
 DT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Mind protein.
 GN MND OR LIN1579.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 NCBI_TaxID=1642;

QY 121 NGCRLQALVDEKWMWNFELICISPRSKLPMGKGAKLGEKVWIDVUGLRLNDVNGLESRVVFDLV 180
 Db 65 ENRCRKLQALIKRKHVNLALIPTAQITRDKNV--KPECMUKLNUELKE---EFDVYI 118
 QY 181 DCAGIDAGFTITAITANEAIVLWTPDITALRDAADVTRGCGIRDKIMVNRTM 240
 Db 119 DCAGIDAGFTITAITANEAIVLWTPDITALRDAADVTRGCGIRDKIMVNRTM 240
 QY 241 IKGEDMSVLDVZEMGLSLSLGVIPDESEVIRSTRGFLVNLKPTL 300
 Db 179 TKKGMLDSDIETLSQLKIGVPPDRNNTVSTNGKGPVILDEKAS-AGQAFRIGRRI 237

Job time : 91 secs

Db 5 IVITSGGGVGKTTSANIGTALALLGKVKVCLVDDIDLRNLDVVMGLENRILYDLDVV 64
 Qy 121 NGDCGLDQALVDPWMSNFELLCISKPSSLKPMGFGKALEWLVDAIKTRPBGSPPFII 180
 Db 65 EGRCRCLKQALIKDKRFFCNCNLLPAQTKK--SAVTPEQMKELVEIKQ---EYVYLI 118
 Qy 181 DCPAGIDAGFTATTPANEAVLVTDPITALRDADRVTLGKLECDGFDIKMIVNRVRTDM 240
 Db 119 DCPAGIEQGKNAVAGDRAIVWTPPELISSVRDADRIGLLEKEVEAPRLVNRGRHM 178
 Qy 241 IKGEBNMSVLDVQENLGLSLGVPEDSEVIRSNRGPPLWINKPPTLAGLAFEQAWRL 300
 Db 179 MRNGEMLDVEIIVIALELLGIVDENVKFSNKGEPIALH-POSKASVAYRNARRI 237
 Qy 301 VEQDSMKAVWEEPEKKRPFSSFG 325
 Db 238 IGETVPLMSFFEQEKVAKTIFSFEG 262
 -

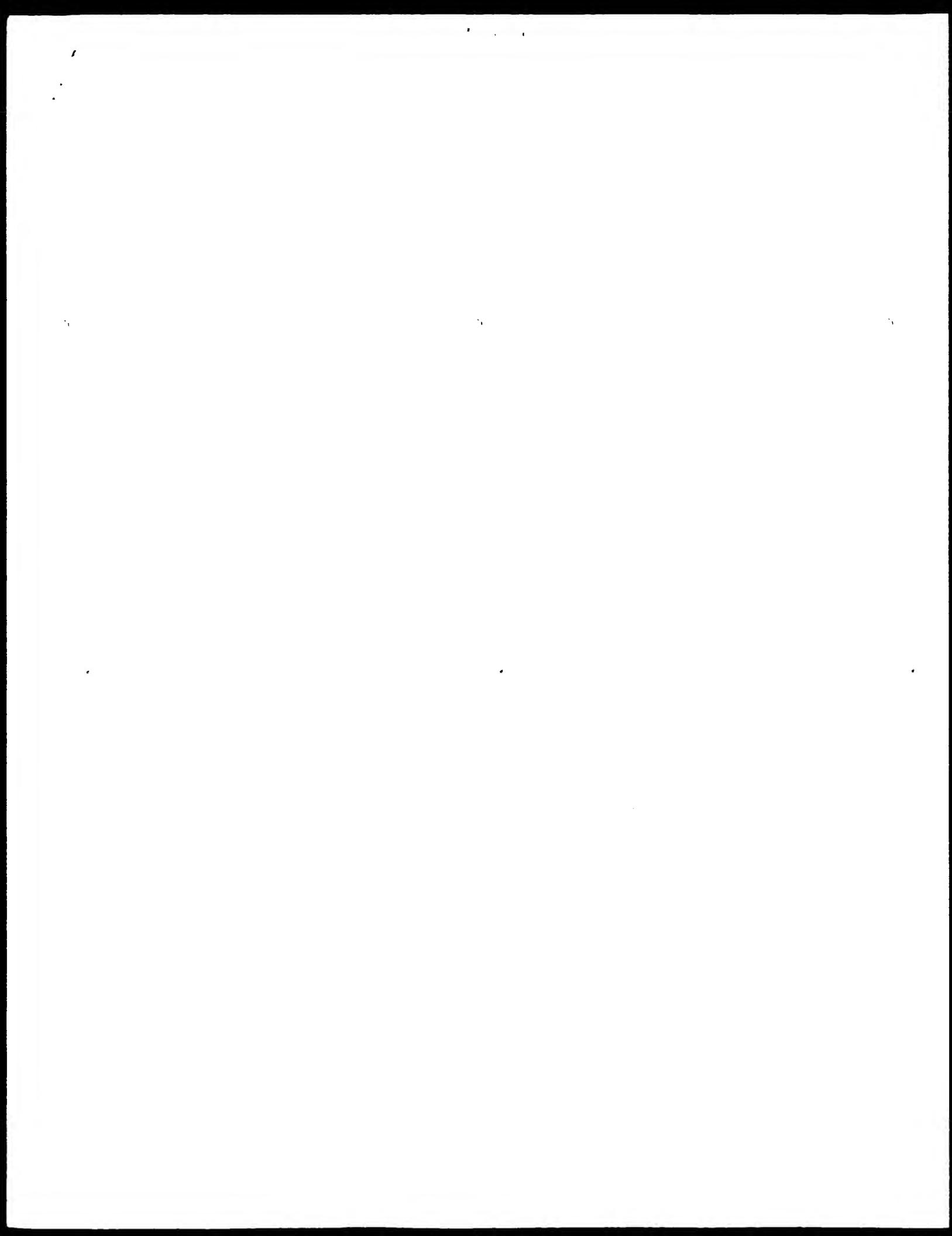
RESULT 15

067033 PRELIMINARY; PRT; 262 AA.
 ID 067033;
 AC 067033;
 DT 01-AUG-1998 (TREMBrel. 07, last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, last annotation update)
 DE Septum site-determining protein MIND.
 GN MIND2 OR AQ_877.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VP5;
 PX MEDLINE=90196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 Graham D.E., Overbeek R., Sneath M.A., Keller M., Ajay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus";
 RL Nature 322:353-358 (1990).
 DR EMBL; AE000712; AAC06996.1; -.
 DR InterPro; IPR00707; ATPase_Para.
 DR Pfam; PF00991; Para; 1.
 KW complete proteome.
 SQ SEQUENCE 262 AA; 28913 MW; 535C2E5F3C5B352A CRC64;

Query Match: 31.2%; Score 516; DB 16; Length 262;

Best Local Similarity 41.4%; Pred. No. 1.7e-34;
 Matches 108; Conservative 65; Mismatches 70; Indels 18; Gaps 3;

Qy 60 IVITSGGGVGKTTSANIGTALALLGKVKVCLVDDIDLRNLDVVMGLENRILYDLDVV 119
 Db 4 VIVITSGKGVGKTTTANIGTALKLIDADIGLRLNDLIGLGERVNYCDEV 119
 Qy 120 INGPCLDQALVDRKRSNSFELLCISKPSSLKPMGFGKALEWLVDAIKTRPBGSPPFII 179
 Db 64 LEGRVYKEALKVDKRGLSILWLLPANQRANKQVTDIE---KWNKTVETIKNSGNYDYL 119
 Qy 180 IDCPIGIDAGFTATTPANEAVLVTDPITALRDADRVTLGKLECDGFDIKMIVNRVRTD 239
 Db 120 VDSPRPIEKGFOTAVSPADKALIIVNPENPQFQDADRIVLIGLLESMKGRNYKIVNIRKWE 179
 Qy 240 MIKGEDMMSVLDVQEMGLSLLGVIPDESEVIRSTNGFPLWINKPPTLAGLAFEQAA 297
 Db 180 MVKGSGAMLSVETIDVILKAEIGIIPERPKLVDFTNCEPITVDFEPFASOII---- 233
 Qy 298 WRLVQDSMKAVWEEPEKKR 318
 Db 234 -----DTARRLMGESIPLKR 248



RESULT 5

US-09-738-626-6925

; Sequence 6925, Application US/09738625

; Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI

APPLICANT: MIZOGUCHI, HIROSHI

APPLICANT: ANDO, SEIKO

APPLICANT: HAYASHI, MIKIRO

APPLICANT: OCHIAI, KEIKO

APPLICANT: YOKOI, HARUHIKO

APPLICANT: TATEISHI, NAOKO

APPLICANT: SENOH, AKIHIRO

APPLICANT: IKEDA, MASATO

APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738,626

CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: JP 00/280988

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS.: 7059

SOFTWARE: PatentIn ver. 3.0

SEQ ID NO: 6925

LENGTH: 279

TYPE: PRT

ORGANISM: Corynebacterium glutamicum

US-09-738-626-6925

Query Match 11.9%; Score 197 5; DB 9; Length 279; Best Local Similarity 26.4%; Pred. No. 3.6e-11; Matches 71; Conservative 46; Mismatches 109; Indels 43; Gaps 10;

Query 58 PRIVWITSGKGGVKTITANVLSLARYGFSTVATADIGERNLNLGLGENV-NYTC 116

Db 7 PRLLITANQGGVKTITANVLSLARYGFSTVATADIGERNLNLGLGENV-NYTC 116

Query 117 VEVINGCRLQALVDRKRSNFEELCISKPRSKLPMCGFGKALEN-----LVDAL 167

Db 66 YELLIGECTADEAM--QPSNTANENLFCI----PATLDLAGEIELVLSVREYRLDAL 118

Query 168 KTR-PEGSPDFIIDCPCAGIDAGFIFTAIPANEAVLAVTPDITAIARDADRTVGLICDG 225

Db 119 GREFLKDHOFDYMICPISIGLITINAMTANEVLPICYYALEGVQL---LNN 173

Query 226 IRDTKMRV-----VRTDMKGDMMSVLDVDEMLGSLLG-VIPDESEVI 271

Db 174 ITMIRQHNLNQLHISAILTMDARTNIAE---QVATEVNDHFGVVLGKRPKPSVKV 229

Query 272 RSTNRGFPVLNRPPTLAGFQAANRL 300

Db 230 EAPGPGQTVIEYDGGSGAMAYLLDAKEL 258

RESULT 6

US-09-712-363-192

; Sequence 192, Application US/09712363

; Patent No. US2002016588A1

; GENERAL INFORMATION:

; APPLICANT: Eisenberg, David

; APPLICANT: Rotstein, Sergio H.

APPLICANT: Marcotte, Edward M.

TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

FILE REFERENCE: 07419-03-2001

CURRENT APPLICATION NUMBER: US/09/712,363

CURRENT FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: PCT/US00/02246

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/117,531

PRIOR FILING DATE: 2000-02-01

PRIOR APPLICATION NUMBER: 60/117,844

PRIOR FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 60/118,206

PRIOR FILING DATE: 1999-02-01

PRIOR APPLICATION NUMBER: 60/126,593

PRIOR FILING DATE: 1999-03-26

PRIOR APPLICATION NUMBER: 60/134,093

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 60/134,092

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 60/165,124

PRIOR FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/165,086

PRIOR FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS.: 292

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 192

LENGTH: 390

TYPE: PRT

ORGANISM: Mycobacterium tuberculosis

US-09-712-363-192

Query Match 11.5%; Score 190; DB 9; Length 390; Best Local Similarity 24.0%; Pred. No. 3e-10; Matches 68; Conservative 58; Mismatches 117; Indels 40; Gaps 9;

Query 32 VNNPSRSPRSPIVSLQPN-RKPELAGETP---RIVVITSGKGGVKTITANVGLSARY 86

Db 95 VMSDDEPDTTELKRQGDTREPVPAQPSLSTRYAVASGKGSVSKVTVNLAAMAVR 154

Query 87 GTSVVAATDADIGRNLDLGLENRNYTCVEVINGCRLQALVDRKRSNFEELCISK 146

Db 155 GLSIVGVLDAIDHGHSIPRMGTTDRPTQV-----ESMILPPIAHQVKVISAQ 202

Query 147 -PRSKLPMGFGSKL-----EWLWALKTRPGEPPDFIIDCPCAGID--AGEITAITPAN 198

Db 203 FTGQNTFVWWRQPMHLAQOQFLALVY---WGDUDVLLDPLPFTGDAVLSVQLPNA 258

Query 199 EAVLWTPDITAIARDADRTVGLICDGIDKIMVNRPTDMKGDMMSVLD---VQ 253

Db 259 EZLWVTFQCLAAEVAERASSIA-LGTRQITVGVVNSLTLT-PRITM-IVFEGGGRLVA 318

Query 254 EMIG-----LISLGVIPEDSEVIRSTRNRGFPVLNKPTLAG 290

Db 319 ERLSRAVGADVPLGQIPUDPALVAGDSDGVPLVLSLSSDSAIG 361

RESULT 7

US-10-102-806-730

; Sequence 730, Application US/10102806

; Publication No. US20030054421A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: P103PC1

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS. 846
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO. 730
 LENGTH: 288
 TYPE: PRT
 ORGANISM: Homo sapiens
 i-US-10-102-805-730

Query Match 10.6%; Score 176; DB 9; length 288;
 Best Local Similarity 22.8%; Pred No. 4.5e-09; Matches 68; Conservative 53; Mismatches 135, Indels 42; Gaps 8, Qy 88 FSVVADADGURNILDLLGLENRNYTCTEVINGCDRLQALVDRKNSNFELCISAF 147
 Db 61 KPGVGTIVNVLCPSPISPRMLGAQGRAVHQC 147
 Qy 148 RSKLPGMF----GGAKLEWLVDALKTRPEGSIDPDFIIDCPACID--AGFT 192
 Db 104 ISUMSUQFLNFKPDEAVWMPSPKPNALIKQFVSDVAGELDLYVUDTPQOTSDEHMATE 163
 Qy 191 AITPANE--AVIYTTPDITALRDAEVGTLIECDG----PDTMTVAPVPTENMIGEMMSYL 250
 Db 164 AIRPYCPIGALWTVTFQAVSVGDRVPELTFCRTGTLRVMGIVENNSGFTCPHCTCTSVP 223
 Qy 251 -----DVOEMLGLSLGIVGTFEDSEVIRSTNRGFLPLVNLNPPTLAGLAFFQAARLVE 302
 Db 224 SRG3GGEFLAQLAGVPUJGVPLDPALMRTIEGHDFIOEFPGSPAAFTSIAQKILD 281

RESULT 8
 US-09-738-626-4744
 ; Sequence 4744, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENO, AKIHIRO
 ; APPLICANT: INEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738-626
 ; CURRENT APPLICATION NUMBER: US/09/738-626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 3883
 ; LENGTH: 478
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 ; US-09-738-626-3883

Query Match 9.9%; Score 164.5; DB 9; length 478;
 Best Local Similarity 28.6%; Pred No. 1.2e-07; Matches 58; Conservative 34; Mismatches 68; Indels 43; Gaps 10; Qy 41 IRSVLQFNPKPELAGETPRPIVITSGKKG3VKTNTANVLSLAPYFSSVATADFLR 160
 Db 250 LRTNLOEIN----VGSSSSVFISSAMPGEKSSTTSWNLALABAGSRVLAIEADRLP 305
 Qy 101 NLPLLLGLENRNYTCTEVINGCDRLQALVDRKNSNFELCISAF 156
 Db 306 RVSKYLGVEGANGLT--DILISKAFAVNDVL--QPMGRTQIYKL--PAGHIPPNSELLG 359
 Qy 157 GKALEWLVDALKTRPEGSIDPDFIIDCPAGI-----DAGFITA-----PANE 199
 Db 359 SAEMEKVIAEL---EEESFDVYVIIADAPPALAVTDAWIGHKGAGLILIAVAGSSTKPELE 414

Query Match 10.5%; Score 173.5; DB 9; length 375;
 Best Local Similarity 24.3%; Pred No. 1.1e-08; Matches 66; Conservative 53; Mismatches 88; Indels 65, Gaps 13, Qy 55 GETPRIVITSGKGKGKTTTANVGLSRLARYGFSVVAIDGLGRNLNLGLENRNY 114
 Db 110 GSTTRIVAVAVASRGKGVKSMTVNLAALAKRGLSGILDQYHSVPMGSKORPH- 168

RESULT 10

SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 225
TYPE: PRT
ORGANISM: *Streptococcus suis*
FEATURE: misc feature
NAME/KEY: OTHER INFORMATION: CPS2C
US-09-767-041-14

Query Match 7.8%; Score 128.5; DB 10; Length 225;
Best Local Similarity 23.2%; Pred. No. 0.0112; Mismatches 61; Indels 93; Gaps 9;
Matches 56; Conservative 31; Mismatches 61; Indels 93; Gaps 9;

Qy 52 ELAGETPRIVITSSKGKVTTANVGLSARYGFSVAIDALGIRN-----L 102
Db 29 QISGADIKUVGITSVSKNSBGKSTTAASLAIAYARSQYKVLVAD--IRNSYMPGFKPI 86

Qy 103 DLUGIENPNTYKTEVINGRCPLD-----QALVRDKRWSNFEELCISK 146
Db 87 TKTGTLTDPYLAGT-TDLSQCLCDPDIPLVIESGKVSNPFLQSK--NPFENLATE 142

Qy 147 PRSKLPMGRGKALEWLVLDAKTHRPEGSPDFIIDCP---AGDAGETTAIRPANPAVL 203
Db 143 RRYY-----DYLVUDCPLGLVIDAATIAQKCDAMVAV- 176

Qy 204 TTPPTITALRDAVPYGTLECTGPIKMDVNPRTDMDMVSVDQEMGLSLLGV 263
Db 177 -----EAGNVKCSSLKV-----EQLBOTGTPLGV 203

Qy 264 I 264
Db 204 I 204

RESULT 13
US-09-738-626-5070
Sequence 5070, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
PRIORITY NUMBER: 1997-04-18
PRIORITY NUMBER: 60/070,488
PRIORITY NUMBER: 1998-03-30
PRIORITY NUMBER: 0376/97
PRIORITY NUMBER: 1997-04-02
PRIORITY NUMBER: 1277/97
PRIORITY NUMBER: 1997-11-10
PRIORITY NUMBER: 60/044,624
PRIORITY NUMBER: 1997-04-18
PRIORITY NUMBER: 60/070,488
PRIORITY NUMBER: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 94
LENGTH: 308
TYPE: PRT
ORGANISM: *Mycobacterium tuberculosis*
US-09-791-171-94

Query Match 6.5%; Score 107.5; PR 10; Length 308;
Best Local Similarity 21.6%; Pred. No. 0.021; Mismatches 46; Indels 97; Gaps 14;
Matches 61; Conservative 46; Mismatches 61; Indels 97; Gaps 14;

Qy 61 VVITSGKCGVGVTTANVGLSARY-GFSVAIDALGIRN-----DILL 106
Db 61 IAVVGLKGAGKHTTAAAGSLAQFADRLADPSAGNADRVRQSGAATADVIA 120

Qy 107 GLE---NRVN YTCVEVIN----GDCPLDQALVDFWNSNFEELCISKPSKPLMCF 155
Db 121 EKELSHYNDIRAHTSVAVNLEVLAPEYSSQRALSDADW---FIADPASRF--- 171

Qy 156 GGKALELVLDAKTHRPEGSPDFIIDCPA---IDAGETTAIRPANPAVL 211
Db 172 -----YVILVADCGAGFFDPTRGVISTV---SGVVVVAWSVSDGA 209

Qy 212 RDAPRVTGCGLECDGIRPK---MIVNRPVTDIMKGEDMMSLVQEMGLSLLGV 263
Db 210 QQSVALDWLRNNGYQBLASRACVWVHII---MPGPENPVAKBLVRLHREQQYQPGRVV 265

Qy 264 IPEDSEVRSTNRGF---PLVNLKOPTLAGA---FEQAWR 299

-Qy 60 IWTISGKGVGVTTANVGLSARYGFSVAIDAD-----LGLRNLDLGLENR 111

-Qy 60 IWTISGKGVGVTTANVGLSARYGFSVAIDAD-----LGLRNLDLGLENR 111

Db 266 MPWDRHIAAGTEISLDLDPYKRRKYLEAALSDDFERAGR 308

RESULT 15

US-09-791-171-70

; Sequence 70, Application US/09791171

; Patent No. US20020094336A1

; GENERAL INFORMATION:

; APPLICANT: ANDERSEN, Peter

; APPLICANT: NIELSEN, Rikke

; APPLICANT: OETTINGER, Thomas

; APPLICANT: RASMUSSEN, Peter Birk

; APPLICANT: ROSENKRANS, Ida

; APPLICANT: WELDINGH, Karin

; APPLICANT: FLORIO, Walter

; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS

; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS

; CURRENT APPLICATION NUMBER: US/09/791,171

; CURRENT FILING DATE: 2001-02-20

; PRIOR FILING DATE: 1998-03-30

; PRIOR APPLICATION NUMBER: 09/650,739

; PRIOR FILING DATE: 1997-04-02

; PRIOR APPLICATION NUMBER: 1277/97

; PRIOR FILING DATE: 1997-11-10

; PRIOR APPLICATION NUMBER: 60/044,624

; PRIOR FILING DATE: 1997-04-10

; PRIOR APPLICATION NUMBER: 60/070,489

; PRIOR FILING DATE: 1998-01-05

; NUMBER OF SEQ ID NOS: 173

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 70

; LENGTH: 666

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

; US-09-791-171-70

; Query Match

; Best Local Similarity 6.5%; Score 107.5; DB 10; Length 666;

; Matches 61; Conservative 46; Mismatches 97; Indels 79; Gaps 14;

; QY 61 WVIISGKSGVGKTTTANGLSARY-GFSVVAIDASIGLRN-----DLI 106

; DB 419 IAVVGLKGGAKGKTTLAALGSLTAQVADRILALADPGAGNLADRVGROSATIAADVLA 478

; QY 107 GLE---NRVN-YTCVEVIN-----GICRLQALVADKRMNFELICISKPRSKLPMGF 155

; DB 479 EKELSHYNDIARHTSVNAYNLEVLPAPPEYSSAQRALSDADWH----FIADPASSR--- 529

; QY 156 GGKALEWLVDALKTRPREGSPDFIIIDCPAG---IDAGFITAITPANEAVIUTTPDITAL 211

; DB 530 -----YNUVLADCGAGFPDPPLIRGVLSV--SGVWVASVSDGA 567

; QY 212 RDARRVTVGLECRDIRK---MINVNRVTDMIKEDMMMSYLDV---DEMLGSSLLGV 263

; DB 568 QQABVALDWLRNQYQDLASRACWVNH-----MPGEFPNVAVKDLVRHFEQVQPGRVVV 623

; QY 264 IPESESEVIRSTNQGF---PLVUNKPPLLAGA---FEQAMR 299

; DB 624 MPWDRHIAAGTEISLDLDPYKRVVFLAALSDDFERAGR 666

Search completed: April 16, 2003, 09:09:25
Job time : 22 secs

